```
(without alignments)
490.775 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | Siziosia de la company | Siziosia del company | Siziosia de la company | Siziosia del company | Siziosia de la company 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA2000.DAT:*/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA2001.DAT:*/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA2002.DAT:*/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA2003.DAT:*/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA2003.DAT:*
                                                                                                                                                                                                                                                                     September 26, 2003, 17:14:42; Search time 67 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MHILKGSPNVIPRAHGQKNT.....TRLTRLSITNETFRKTQLYP
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1107863 seqs, 158726573 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Listing first 45 summaries
                                                                                                                                                                                OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A_Geneseq_19Jun03:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Post-processing: Minimum Match 08
Maximum Match 1008
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-852-100A-2
1439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BLOSUM62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               112.
113.:..
116.:..
116.:..
116.:..
127.:..
223.:..
24.:.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Database
                                                                                                                                                                                                                                                                          Run on:
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

			Description	Tiology when a comment	Human beta-amyloid	Human BBP-1 protei	Human 5' EST secre	Extended human sec	Human 5' EST secre	Drosophila melanoq	RNA polymerase II	Human secreted pro
SUMMARIES			ID	AAW94291	AAY70759	AAE33877	AAY12358	AAY36021	AAY12426	ABB65236	AAU97631	ABR47818
				20	5	24	20	20	20	22	23	24
			Match Length DB	269	269	269	139	162	148	178	100	221
	æ	Query	Match	100.0	100.0	100.0	52.0	46.8	46.4	23.5	20.4	14.0
			Score	1439	1439	1439	748	673.5	667.5	338	293	201
		Result	NO.		7	m	4	Ŋ	9	7	60	6

Human gene 102 enc Human secreted pro Human beca amyloid Human Amyloid Apop A human IANGO 223 A human IANGO 223	human TANGO 2 NA encoding a rosophila mela uman secreted	cance phila guanc polyp pciyp	Human polypeptide Human secreted pro Human secreted pro Rat protein isolat Human vesicle-asso Human polypeptide Novel human diagno Human BBP-1 protei	
ABR00112 AAY27658 AAY70761 ABR48493 AAB08641 AAB08656	365 364 361 37 35 35	357 347 347 357	037 527 527 527 529 529 529 530 530 530	00000000000000000000000000000000000000
220 221 221 221 221	222222	22222	2222222 20222222	22 22 20 21 71 21 24
~1~~~~~	* ** * * * * * * * * * * * * * * * * * *	77775	171 172 140 2140 2444 68	316 316 764 764 310 338 338 576
				, re
201 200 200 200 200 200	200 200 196 182 138.5	(7)	121 121 119 119 95.5 90.5 88.5	90 00 00 00 00 00 00 00 00 00 00 00 00 0
10 11 11 11 12 13 13 13 14	10 10 10 10 10 10 10 10 10 10 10 10 10 1	23 24 25 27 28	31 0 14 0 16 16 16 16 16 16 16 16 16 16 16 16 16	0 W W W 4 4 4 4 4 4 9 10 10 10 10 10 10 10 10 10 10 10 10 10

ALIGNMENTS

```
Beta-amyloid peptide binding protein; BBP; beta-amyloid protein; BAP; human; Alzheimer's disease.
                                                                                                                       Jacobsen JS, Kajkowski EM, Ozenberger BA;
                                                             Human beta-amyloid peptide-binding protein (BBP).
                                                                                                                  Location/Qualifiers
              AAW94291 standard; Protein; 269 AA
                                                                                                                                                                                                                       (AMHP ) AMERICAN HOME PROD CORP.
                                                                                                                                                                                        98WC-CS07462.
                                                                                                                                                                                                        97US-0064583.
                                              (first entry)
                                                                                                   Homo sapiens
                                                                                                                                                         W09846635-A2
                                                                                                                                                                                        14-APR-1998;
                                                                                                                                                                                                       .6-APR-1997;
                                             27-APR-1999
                                                                                                                                                                         22-0CT-1998
                                                                                                                                                                                                                                       Bard JA, J
Walker SG;
                             AAW94291;
                                                                                                                   Key
Region
RESULT 1
```

~

```
13-OCT-1998;
                                                                                          13-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     diagnostics.
                                                                20-APR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            241
    Doma in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAE33877
    Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ें
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                            The present sequence represents a beta-amyloid peptide binding protein (BBP). The polynucleotide comprising the entire BBP nucleotide sequence of clone BBP1-Ii is deposited under the accession number ATCC 98617. The polynucleotide comprising a fragment of BBP (nucleotides 202-807 of the full length BBP) of clone pEK196 is deposited as ATCC 98395. Host cells transformed with a vector comprising the BBP nucleic acid are used for the recombinant production of the protein. The protein can be used in a method for diagnosing a disease characterised by aberrant expression of human beta-amyloid protein (BAP). The protein can also be used in a method for screening for compounds which regulate expression of a BAP binding protein. The proteins, antibodies and identified compounds can be used in the treatment or prevention of Alzheimer's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                         123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 KDPKINDATQEPVNCTNYTAHVSCFPAPNITCKDSSGNETHFTGNEVGFFKPISCRNVNG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YSYKVAVALSLFLGWLGADRFYLGYPALGLLKFCTVGFCGIGSLIDFILJSMQIVGPSDG 240
                                                                                                                                                                                                                                                                                                                                                                            9
                                                                                                                                                                                                                                                                                                                                                                                                  1 MHILKGSPNVIPRAHGOKNTRRDGTGLYPMRGPFKNLALLPFSLPLLGGGGSGSGEKVSV 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         199..201
/label- DRF_motif
/note= "Substitution of the Arg abrogates protection"
                                                                                                                                                                                                                                                                                                                                                                         1 MHILKGSPNVIPRAHGQKNTRRDGTGLYPMRGPFKNLALLPFSLPLLGGGGSGGSGEKVSV
                                                                                                                                                                                                                                                                                                                                                                                                                             SKMAAAMPSGPSAPEAVTARLVGVLWFVSVTTGPWGAVATSAGGEESLKCEDLKVGQYIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Beta-amyloid peptide binding protein; BBP; BAP; tumour; suppresser; G-protein coupled receptor; GPCR; integral membrane protein; antiqen; neuronal cell; nonhuman primate; NHP; G-protein signalling pathway; apoptosis; immunogen; therapeutic; treatment; prevention; diagnostic.
                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                       100.0%; Score 1439; DB 20; Length 269; 100.0%; Pred. No. 9.4e-142; ive 0; Mismatches 0; Indels 0;
                                                 Polynucleotide encoding beta-amyloid peptide binding protein to identify inhibitors of beta-amyloid peptide for treating Alzheimer's disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human beta-amyloid peptide (BAP) binding protein, BBFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /label- Transmembrane_domain_l
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SSYIIDYYGTRLTRLSITNETFRKTQLYP 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                241 SSYIIDYYGTRITRESITNETFRKTQLYP 269
                                                                                                   Claim 7; Pages 43-44; 59pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY70759 standard; Protein; 269 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                   Local Similarity 100.
nes 269; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     177..198
              WPI; 1999-080736/07
                                                                                                                                                                                                                                                                                                269 AA;
                          N-PSDB; AAX05735
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24-JUL-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                     61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181
                                                                                                                                                                                                                                                                                                  Sednence
                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY70759;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Domain
                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 2
AAY70759
ò
                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                           δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  õ
```

```
The present sequence is the beta-amyloid peptide (BAP) binding protein-1 (BBP1). It is an integral membrane protein, that traverse the membrane twice. It is related to G protein-coupled receptor (GPCR) protein superfamily. It interacts with G-alpha proteins and regulates the activity of G-protein signalling pathways. BBP genes are widely expressed in neuronal cells of nonhuman primate (NHP) brain and overexpressed in some tumours. It functions as a suppressor of apoptosis induction. BBP proteins are used as immunogens to raise antibodies, useful as therapeutics and as antigens in solid phase assays. They are also useful as reagents to identify molecules which effect the interaction of BBP and a cloned protein, that are useful in the treatment or prevention of diseases, associated with apoptosis. The polynucleotides are useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SKMAAAWPSGPSAPFAVTARLVGVLWFVSVTTGPWGAVATSAGGEESLKGEDLKVGQY1C 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KDPKINDAT@EPVNCTNYTAHVSCFPAPNITCKDSSGNETHFTGNEVGFFKPISCRNVNG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YSYKVAVALSLFLGWLGADRFYLGYPALGLLKFCTVGFCGIGSLIDFILISMQ1VGPSDG 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Note: In claim 5, the patent claims an amino acid sequence from figure 2. However, figure 2 does not contain any sequence. It is inferred from the disclosure that the figure 2 sequence refers to BBP1 protein, shown in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MHILKGSPNVIPRAHGOKNTRRDGTGLYPMRGPFKNLALLPFSLPLLGGGGSGSGKVSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel 3-protein-coupled receptor-like proteins and polynucleotides useful for regulating apoptosis, comprises integral membrane protein traversing the membrane twice
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 269;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 1439; DB 21; 100.0%; Pred. No. 9.4e-142;
/label= Tramsmembrane_domain_2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SSYIIDYYGIRLIRLSIINETFRKIQLYP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CF)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 1; Page 62-63; 68pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAE33877 standard; Protein; 269 AA
                                                                                                                                                                                                                                                                                                                                                                                                      S
                                                                                                                                                                                                                                                                                                                                    (AMHP ) AMERICAN HOME PROD CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ..
                                                                                                                                                                                                                                                                                                                                                                                                      Ozenberger BA, Kajkowski EM,
                                                                                                                                                                                                   99WC-US21621
                                                                                                                                                                                                                                                                  98US-0104104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2000-317982/27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 269: Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         269 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; AAZ52369
                                                              W0200022125-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              this sequence
```

0

us-09-852-100a-2.rag

(first entry)

```
17-JUN-1999
  AAY12358;
  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .
;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SKMAAAWPSGPSAPEAVTARLVGVLWFVSVTTGPWGAVA~SAGGEESLKCEDLKVGGYIC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KDPKINDATQEPVNCTNYTAHVSCFPAPNITCKDSSGNETHFTGNEVGFFKPISCRNVNG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 181 YSYKVAVALSLFLGWLGADRFYLGYPALGLLKFCTVGFCGIGSLIDFILISMQIVGPSDG 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 SKMAAAWPSGPSAPEAVIARLVGVLWFVSVITGPWGAVATSAGGEESLKCEDLKVGQYIC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MHILKGSPNVIPRAHGQKNIRRDGTGLYPMRGPFKNLALLPFSLPLLGGGGSGSGEKVSV 60
                                                                                                                                                                                                                                                                                                                                               The present invention relates to novel human beta-amyloid peptide (BAP) Abeta, betaAP)-binding (BBP) proteins and polynucicchides encoding such proteins. BBP sequences are useful to diagnose and/or treat diseases associated with aberrant expression of human BAP such as Alzheimer's disease (AD). They are used to generate transgenic animals. Sequences of the invention are also used in gene therapy. The present sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New human beta-amyloid peptide-binding protein, useful for diagnosing and/or treating diseases associated with aberrant expression of beta-amyloid peptide, e.g. Alzheimer's disease
                                                         Human; beta-amyloid peptide-binding protein; BAP; Abeta; betaAP; BBP;
Alzheimer's disease; AD; transgenic; transgenic animai; gene therapy;
neuroprotective; nootropic.
                                                                                                                                                                                                                            SG
                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 1439; DB 24; Length 269; ilarity 100.0%; Pred. No. 9.4e-142; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                            Walker
                                                                                                                                                                                                                            Jacobsen JS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SSYIIDYYGTRLTRLSITNETFRKTQLYP 269
                                                                                                                                                                                                                            Kajkowski EM,
                                                                                                                                                                                                                                                                                                                              Claim 4; Page 84-85; 85pp; English
                                                                                                                                                                        7
                                                                                                                                                                06-MAY-2002; 2002WO-US14223.
                                                                                                                                                                                   09-MAY-2001; 2001US-0852130.
                     (first entry)
                                                                                                                                                                                                                            Bard JA,
                                                                                                                                                                                                                                                                                                                                                                                                            is human BBP-1 protein.
                                                                                                                                                                                                                          Ozenberger BA, Bard J
Sofia HJ, Howland DS;
                                        Human BBP-1 protein.
                                                                                                                                                                                                                                                         WPI; 2003-120537/11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
les 269; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                269 AA;
                                                                                                                                                                                                                                                                 N-PSDB; AAD51940
                                                                                                                       WO200290499-A2
                                                                                                                                                                                                        (AMEP ) WYETH.
                                                                                                     Homo sapiens
                     02-MAY-2003
                                                                                                                                           14-NOV-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                               Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
AAE33877
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Loca
Matches
ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ď
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
```

AAY12358 standard; Protein; 139 AA.

RESULT 4
AAY12358
ID AAY1

```
can also be used for producing secreted proteins, and encode the proteins given in AAY1261 to have secreted proteins, and encode the proteins given in AAY1261 to AAY12514, respectively. The proteins given represent the signal peptide and an N-terminal fragment of a secreted protein. The nucloic acid sequences can be used for producing secreted human gene products. They can also be used to develop products for diagnosis and therapy. The proliferation/differentiation activity, heam topologis regulating activity, chemication activity, heam topologis regulating activity, chemicatoric/chemokinetic activity, anti-inflammatory activity, tumour inhibition activity or other activity, anti-inflammatory activity, tumour inhibition activity or other activity anti-inflammatory activity, tumour inhibition activity or other activities. The products can be used in forensic, gene therapy and chromosome mapping procedures. The sequences can also be used for obtaining corresponding promoter sequences. The nucleic acids encoding the signal peptide can be used for directing extracellular secretion of a polypeptide or the inscript of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                63 MAAAWPSGPSAPEAVTARLVGVLWFVSVTTGPWGAVATSAGGEESLKCEDLKVGQYICKD 1223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   123 PKINDATQEPVNCTNYTAHVSCFPAPNITCKDSSGNETHFTGNEVGFFKPISCRNVNGYS 1823
                                                                                                      forensic; gene therapy; chromosome mapping; signal peptide; upstream regulatory sequence; cytokine activity; cell proliferation: differentiation; haematopoisesis regulation; tissue growth regulation; reproductive hormone regulation; chemotactic; chemokinetic; haemostatic; thrombolytic; anti-inflammatory; tumour inhibition.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  polypeptide into a membrane, or importing a polypeptide into a cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New nucleic acids encoding human secreted proteins - obtained from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cDNA libraries prepared from e.g. liver, ovary, brain, prostate, kidney, lung, umbilical cord, placenta and colon tissue
                                                                        Human; secreted protein; EST; expressed sequence tag; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            52.0%; Score 748; DB 20; Length 139; 99.3%; Pred. No. 6.2e-70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Œ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lacroix
Human 5' EST secreted protein SEQ ID NO:389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 27; Page 714-715; 824pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Dumas Milne Edwards J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YKVAVALSLFLGWLGADRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98WO-IB01222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9708-0905135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1999-153778/13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 138; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           139 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB: AAX41191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (GEST ) GENSET
                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                           WO9906548-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Duclert A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ŏ
```

us-09-852-100a-2.rag

```
AAY12426 standard; Protein; 148 AA
                                                                      17-JUN-1999
                                                                                                                                                                                                                                                   11-FEB-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Seguence
                                               AAY12426;
RESULT 6
           AAY12426
                                   ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This sequence is encoded by an extended human secreted protein coding sequence of the invention. The secreted proteins can be used in treating or controlling a variety of human conditions. The secreted proteins may act as cytokines or may affect cellular proliferation or differentiation or may act as immune system regulators, haematopolesis regulators, tissue growth regulators, regulators of reproductive hormones or cell movement or have chemotactic/chemokinetic, receptor/ligand, anti-inflammatory or tumour inhibition activity. The DNAs can be used in forensic procedures to identify individuals or in diagnostic procedures to identify individuals or in diagnostic procedures to identify the genes corresponding to the extended colons. They are also useful for constructing a high resolution map of the human chromosomes. They can also be used for gene therapy to control or treat genetic diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     63 MAAAWPSGPSAPEAVIARLVGVLWFVSVTTGPWGAVATSAGGEESLKCEDLKVGQYICKD 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        123 PKINDATQEPVNCTNYTAHVSCFPAPNITCKDSSGNETHFIGNEVGFFKPISCRNVNGYS 182
                                                                                                                    protein; human; cytokine; cellular proliferation; cell movement;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MAAAWPSGPXAPEAVTARLVGVLWFVSVTTGPWGAVATSAGGEESLKCEDLKVGQYTCKD 60
                                                                                                                             cellular differentiation; immune system regulator; anti-infiammatory; haematopoiesis regulator; tissue growth regulator; tumour inhibitor; reproductive hormone regulator; chemotaxis; chemokinesis; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ë.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 673.5; DB 20; Length 162;
Pred. No. 4.8e-62;
4; Mismatches 17; Indeis 3;
                                                                                            Extended human secreted protein sequence, SEO ID NO. 406
                                                                                                                                                                                                                                                                                                                                                                      Bougueleret L, Duclert A, Dumas Milne Edwards J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 9; Page 346-347; 516pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated human secreted proteins
                      AAY36021 standard; Protein; 152 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          45.8%;
84.1%;
                                                                                                                                                                                                                                                                                     980S-0095116.
                                                                                                                                                                                                                                                                                                            98US-0074121.
                                                                                                                                                                                                                                                             98WO-IB02122
                                                                      13-SEP-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  127; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1999-385906/32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   162 AA;
                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; AAX97705
                                                                                                                                                                   genetic disease
                                                                                                                                                                                                                                                                                                                                                (GEST ) GENSET
                                                                                                                                                                                          Homo sapiens.
                                                                                                                                                                                                                W09931236-A2
                                                                                                                                                                                                                                                               17-DEC-1998;
                                                                                                                                                                                                                                                                                     10-AUG-1993;
17-DEC-1997;
                                                                                                                                                                                                                                                                                                                         13-APR-1998;
                                                                                                                                                                                                                                                                                                            09-FEB-1998;
                                                                                                                                                                                                                                       24 - JUN - 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Seguence
                                               AAY36021;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                     Secreted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
           AAY3602
                                   셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         õ
```

61

a ò

```
5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    123 PKINDATGEPVNCTNYZAHVSCFPAPNITCKDSSGNETHFTGNEVGFFKPISCRNVNGYS 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 PKINDATQEPVNCTNYTAHVSCFPAPNITCKDXSGNETHFIGHTHHHHHHHHHHHHHHHHH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           human secreted proteins, and encode the proteins given in AAV12261 to AAV12361, respectively. The proteins given represent the signal peptide and an N-terminal fragment of a secreted protein. The nucleic acid sequences can be used for producing secreted human gene products. They proteins obtained may have cytokine activity, cell proliferation/differentiation activity, haematopolesis regulating activity, tissue growth regulating activity, haematopolesis regulating activity, receptor/ ligand activity, anti-inflammatory activity, tumour inhibition activity or other activity anti-inflammatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               can be used in forensic, gene therapy and chromosome mapping procedures. The sequences can also be used for obtaining corresponding promoter sequences. The nucleic acids encoding the signal peptide can be used for directing extracellular secretion of a polypeptide or the insertion of a polypeptide into a membrane, or importing a polypeptide into a cell.
                                                                                                                                                                       forensic; gene therapy; chromosome mapping; signal peptide; upstream regulatory sequence; cytokine activity; cell proliferation; differentiation; haematopolesis regulation; tissue growth regulation; reproductive hormone regulation; chemotactic; chemokinetic; haemostatic; thirombolytic; anti-inflammatory; tumour inhibition.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    63 MAAAWPSGPSAPEAVTARLVGVLWFVSVTTGPWGAVATSAGGEESIKCEDLKVGQYICKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MAAAWPSGPXAPEAVIARLVGVLWFVSVTTGPWGAVATSAGGEESLKCEDLKVGQYICKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAX41094 to AAX41347 represent 5' expressed sequence tags (ESTs) tor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New nucleic acids encoding human secreted proteins - obtained from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cDNA libraries prepared from e.g. liver, ovary, brain, prostate, kidney, lung, umbilical cord, placenta and colon tissue
                                                                                                                                                Human; secreted protein; EST; expressed sequence tag; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 148;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 46.4%; Score 667.5; DB 20; Lengun
B3.3%; Pred. No. 1.8e-61;
....matches 18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ä
                                                                        Human 5' EST secreted protein SEQ ID NO:457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lacroix
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    183 YKVAVALSLFLGWLGADRFYLGY-PALGLL 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 27; Page 763-764; 824pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Duclert A, Dumas Milne Edwards J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98WO-IB01222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            97uS-0905135
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Oucry Match 46.4
Best Local Similarity 83.3
Matches 125; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1999-153778/13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               148 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; AAX41259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (GEST ) GENSET
                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C1-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO9906548-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Š
```

```
Mao Y, Xie Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12-JUN-2003
                                                                                                                                                                                                                                                                                                                               CN1331300-A.
                                                                                                                                                                                                                                                                                                                                                                            .6-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sednence
                                                                        AAU97631;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABR47818;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 9
ABR47818
  AAU97631
                          $\circ{\circ}{\circ}$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\ci
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            G
G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signaling and coll-ceil interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaccutical drugs. The invention discloses genomic DNA sequences (ABL16175-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins. The invention the sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at fip.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SLKCEDLK-VGQYICKDP---KINDATQEPVNCTNY-TAHVSCFPAPNITCKDSSGNETH 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NVDCNELQMMGQFMCPDPARGQIDPKTQQLAGCTREGRARVWCIAANEINCTE-TGNAT-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FTGNEVGFFKPISCRNVNGYSYKVAVALSLFLGWLGADRFYLGYPALGLLKFCTVGFCGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14; Gaps
                                                                                                                                                                                                                                                                                                                            developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; SEQ ID NO 22500; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 23.5%; Score 338; DB 22; Length 178; Best Local Similarity 42.6%; Pred. No. 6.5e-27; Matches 69; Conservative 30; Mismatches 49; Indels 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       222 GSLIDFILISMQIVGPSDGSSYIIDYYGTRLTRLSIINETFR 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ID NO 22500
Myers EW;
                                                                                                                                                                                                                                                                            Drosophila melanogaster polypeptide SEQ
                                                                                                                                        Ş
                                                                                                                                      ABB65236 standard; Protein; 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  I.i PWD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23-MAR-2000; 2000US-191637P.
11-JUL-2000; 2000US-0614150.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23-MAR-2001; 2001WO-US09231
                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Adams M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-656860/75.
N-PSDB; ABL09339.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (PEKE ) PE CORP NY
                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200171042-A2.
                                                                                                                                                                                                                                                                                                                                                  pharmaceutical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            interactions
                                                                                                                                                                                                                               26-MAR-2002
                                                                                                                                                                                                                                                                                                                        Drosophila;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Venter JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                    ABB65236;
                                                                                                                ABB65236
                                                                                                                                                                                    Q.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
```

```
Cardiant; antiarrhythmic; antiarteriosclerotic; vasotropic; cytostatic; vulnerary; antiinflammatory; nootropic; neuroprotective; antiparkinsonian; gene therapy; human; cardiovascular disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             polypeptide-RNA polymerase II subunit il protein. The invention also comprisses a process for preparing the polypeptide of the invention by DNA recombination, the application of the polypeptide in treating diseases such as cancer, human immunodeficiency virus (HIV) infection, etc., the antagonist of the polypeptide and its medical action, and the application of the said polynuclectide are disclosed. The present sequence represents the RNA polymerase II subunit II protein of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Polypeptide-RNA polymerase II subunit 11 and polynucleotide for coding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This invention relates to the DNA and protein sequences of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                        RNA polymerase II subunit 11; cancer; HIV; infection; human immunodeficiency virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 293; DB 23;
Pred. No. 1.4e-22;
1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             (BODE-) BODE GENE DEV CO L'TD SHANGHAI.
                                                                                                                               RNA polymerase II subunit 11 protein
  AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Æ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human secreted protein, SEQ ID 709.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; Page 29; 32pp; Chinese.
AAU97631 standard; Protein; 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Protein; 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20.4%;
ilarity 98.2%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                      30-JUN-2000; 2000CN-0116963.
                                                                                                                                                                                                                                                                                                                                                                                                                 30-JUN-2000; 2000CN-0116963
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2002-340664/38
N-PSDB; ABK52558.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
es 55; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABR47818 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200295010-A2.
```

ő

RESULT

9

```
221 AA:
 immune disorder;
                                                                                    WO200275488-A1.
                                                                                                                03-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY27658;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY27658
              ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ωp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     XXXXXX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'n
                                                                                                                                                                                                                                                                              The present invention relates to novel human secreted proteins (ABR47633-ABR40145) and their coding sequences (ACC50344-ACC50856). The proteins and their coding sequences are useful for the preparation of a diagnostic or pharmaceutical composition for diagnosing or treating a cardiovascular disorder (e.g., arrhythmia, tachycardia, cardiac arrest, coronary arteriosclerosis and myocardial ischamnia), neural disorders, immune system disorders, muscular disorders, reproductive disorders, gastrointestinal disorders und/or cancercus diseases and conditions, for proliferative disorders and/or cancercus diseases and conditions, for whound healing and epithelial cell proliferation, to treat inflammation or infection, for treating thrombosis and arteriosclerosis, for preventing neural damage which occurs in neuronal disorders or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        135 CTNYIA--HVSC----FPAPNITCKDSSGNETHFTGNEVGFFKPISCRNVNGYSYKVAVA 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         neurodegenerative conditions such as Alzheimer's disease and Parkinson's disease, to enhance bone and periodontal regeneration and aid in tissue stransplants or bone grafts, to prevent skin aging or hair loss, to stimulate growth and differentiation of haematopoietic cells and bone marrow cells when used in combination with other cytokines, to maintain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            organs before transplantation or for supporting ceil culture of primary tissues, to increase or decrease differentiation or proliferation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human: secreted protein; digestive disorder; gastrointestinal disorder; mouth; oesophagus; stomach; small intestine; large intestine; liver; billary tract; pancreas; cancer; tumour; hyperproilferative disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                189 LSLFLGWLGADRFYLGYPALGLLKFCTVGFCG1GSLIDF1LISMQIVGPSDGSSY: 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Note: The sequence data for this patent was published in electronic format and is available from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        embryonic stem cells, or to modulate mammalian characteristics or
                                                                                                                                                                                              Novel human secreted proteins, useful for detecting, preventing, diagnosing, prognosticating, treating and/or ameliorating cardiovascular disorders such as arrhythmia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human gene 102 encoded secreted protein HMEED13, SEQ ID NO:401.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14.0%; Score 201; DB 24; Length 22;; 45.7%; Pred. No. 1.9e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              39; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12: Mismatches
                                                                                                                                                                                                                                                         Claim 13; SEQ ID 709; 1881pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABR00112 standard; Protein; 221 AA
                                                                                                                (HUMA-) HUMAN GENOME SCI INC
                            19-MAR-2002; 2002WO-US09785
                                                        2001US-277340P.
                                                                     19-JUL-2001; 2001US-306171P.
13-NOV-2001; 2001US-331287P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         03-APR-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             53; Conservative
                                                                                                                                                                     WPI; 2003-129429/12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         221 AA;
                                                        21-MAR-2001;
28-NOV-2002
                                                                                                                                          Rosen CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABR00112:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABR00112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
```

```
protein genes, and AbP00011-ABP00299 represent the proteins they encode.

Charaty-Assals 1540 represent thuman secreted proteins they encode.

ABZ11479-ABZ1540 represent thuman secreted proteins they encode.

Charaty-Assals 1540 represent thuman secreted proteins they encode.

Convention also encompasses antibodies specific for the secreted proteins. The secreted proteins in drug screening, and recombinant vectors and host cells comprising a nucleic acid of the invention. The secreted proteins, nucleic acids encoding them, antibodies or antibody fragments specific for the secreted proteins, and modulators of protein activity are useful for diagnosing, treating, amelicarating or preventing dispessive disporders. Such conditions include disporders of the mouth, cesophagus, stomach, small intestine, large intestine, liver, biliary tract and pancreas, and include cancers of these organs and tissues. The creatment of immune disporders, and to promote wound healing. Nucleic acid: hyperproliferative disorders, and to promote wound healing. Nucleic acid: hyperproliferative disorders, and to promote wound healing. Nucleic acid: of the invention may be used for chromosome identification, chromosome condapping, in gene therapy, for identifying individuals from minute to bological samples, as hybridisation probes, and as molecular weight invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 35 CTNYTA--HVSC----FPAPNITCKDSSGNETHFTGNEVGFFKPISCRNVNGYSYKVAVA 183
inflammation; infection; wound healing; drug screening;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               112 CINSTSCMTVSCPRQRYPA-NCTVRD----HVHCLGNRT-FPKMLYCNWTGGYKWSTALA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New human secreted proteins and nucleic acids, useful for detecting, preventing, diagnosing, prognosticating, treating and/or ameliorating e.g. gastrointestinal diseases and disorders, or cancers -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels 12; Gaps
                                            chromosome identification; chromosome mapping; cytostatic; antiinflammatory; immunosuppressive; vulnerary; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
14.0%; Score 201; DB 24; Length 221;
Best Local Similarity 45.7%; Pred. No. 1.9e-12;
Matches 53; Conservative 12; Mismatches 39; Indels 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 13; Page 1007; 1216pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY27658 standard: Protein; 222 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19-JUL-2001; 2001US-306171P.
13-NOV-2001; 2001US-331267P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19-MAR-2002; 2002WC-US08276.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-MAR-2001; 2001US-277340P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30-JUL-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rosen CA, Ruben SM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2003-029900/02.
N-PSDB; ABZ71291.
```

```
This sequence represents a secreted human protein encoded by the generate fusion proteins by linking to the gene to a human immunoglobulin for portion (e.g. AAX84924) for increasing the stability of the fused protein as compared to the human protein only.

The invention relates to 125 novel genes and their fragments (mucleic acid sequences: AAX84933.X85057; amino acid sequences AAX97567-Y27933; which are useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. Also, pathological conditions can be diagnosed by determining the amount of the new polypoptides in a sample or by determining the presence of mutations in the new polymucleotides. Specific uses are described for each of the 125 polymucleotides, based on which tissues they are most highly expressed in
                                             diagnosis: tissue, cancer; tumour; neurodegenerative discret; leukaemiu; developmental abnormality; foetal deficiency; blocd; allergy; renai; immune system; asthma: lymphocytic disease; brain; hepatic; lymphoma; inflaumation; ischaemic shock; Albeimer's disease; restenosis; AIDS; cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus; osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion; endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
                                 Human; secreted protein; tusion protein; gene therapy; protein therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New human secreted proteins and coding sequences useful for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      disorders of the immune system and hyperproliferative disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Feng P, Janat F;
i J, Olsen HS, Rosen CA;
Human secreted protein encoded by gene No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ni G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim il; Page 400-40i; 507pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ebner R, Endress GA, Ferafleur DW, Moore PA, Ni J, Shi Y, Soppet DR, Wei Y:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (see AAX84933 for described uses).
                                                                                                                                                                                                                                                                                                                                                               970S-0064911.
970S-0064912.
970S-0064983.
970S-0064984.
970S-00649885.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 97US-0066096.
97US-0066094.
97US-0066095.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                97US-0064987.
97US-0064988.
                                                                                                                                                                                                                                                                                                                                   97US-0064900
97US-0064908
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  97US-0066089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1999-337740/28.
N-PSDB; AAX85024.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lafleur DW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        222 AA;
                                                                                                                                                                                                                  WO9924836-A1.
                                                                                                                                                                                                                                                                                  04-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                              1997:
                                                                                                                                                                                                                                                                                                                   17-NOV-1997
                                                                                                                                                                                                                                                                                                                                                  1997
                                                                                                                                                                                                                                                                                                                                                                07-NOV-1997
07-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                    NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                07-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17 - NOV - 1997
17 - NOV - 1997
                                                                                                                                                                                                                                                 20-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                 NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                 NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                  NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Carter KC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Seguence
                                                                                                                                                                                                                                                                                                                                                    NOV-
```

Best_Local Similarity Matches 53; Conserv

Query Match

```
The present sequence is the beta-amyloid peptide (BAP) binding protein-is (BBP3). It is an integral membrane protein, that traverse the membrane twice. It is related to G protein-coupled receptor (GPCP) protein superfamily. It interacts with G-alpha proteins and regulates the activity of G-protein signalling pathways. BBP genes are widely expressed in neuronal cells of nonhuman primate (MHP) brain and overexpressed in some tumours. It functions as a suppressor of apoptosis induction. BBP proteins are used as immunogens to raise antibodies, useful as proteins are used as antigens in solid phase assays. They are also useful as reagents to identify molecules which effect the interaction of BBP and a cloned protein, that are useful in the treatment or prevention of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       diseases associated with apoptosis. The polynucleotides are useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 135 CINYTA--HVSC----FPAPNITCKDSSGNETHFTGNEVGFFKPISCRNVNGYSYKVAVA
                                                                                                                                                                                                                                                          Beta-amyloid peptide binding protein; BBP; BAP; tumour; suppressor; G-protein coupled receptor; GPCR; integral membrane protein; antigen; neuronal cell; nonhuman primate; MFP; G-protein signalling pathway; apoptosis; immunogen; therapeutic; treatment; prevention; diagnostic.
LSLFLGWLGADRFYLGYPALGILKFCTVGFCGIGSLIDFILISMQIVGPSDGSSYI 244
                   /label- DRF_motif
/note= "Substitution of the Arg abrogates protection"
196..215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel G-protein-coupled receptor-like proteins and polynucleotides useful for regulating apoptosis, comprises integral membrane protein traversing the membrane twice
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 39; Indels 12;
                                                                                                                                                                                                                           Human beta-amyloid peptide (BAP) binding protein, BBP3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13.9%; Score 200; DB 21;
45.7%; Pred. No. 2.4e-12;
ive 12; Mismatches 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /label - Transmembrane_domain_2
                                                                                                                                                                                                                                                                                                                                                                                                                  /label- Transmembrame_domain_1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 1; Page 67-68; 68pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CF.
                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualificrs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ŋ
                                                                                                                     AAY70761 standard; Protein; 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (AMHP ) AMERICAN HOME PROD CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ozenberger BA, Kajkowski EM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 13.9%;
Best Local Similarity 45.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98US-0104104.
                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                   176..178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI: 2000-317982/27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              221 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; AA252371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200022125-A2
                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13-CCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13-OCT-1998;
                                                                                                                                                                                          24-JUL-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20-APR-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         diagnostics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               53;
186
                                99:
                                                                                                                                                        AAY70761;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Seguence
                                                                                                                                                                                                                                                                                                                                                                                                  Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                     Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                   AAY70751
ID AAY
                                                                                                                                        ò
                              3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             135 CINYTA--HVSC----FPAPNITCKDSSGNETHFTGNEVGFFKPISCRNVNGYSYKVAVA 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14.0%; Score 20;; DB 20; Length 222; ilarity 45.7%; Pred. No. 1.9e-12; Conservative 12; Mismatches 39; Indels 1;
```

a ò

```
proliferative disorder neoplasm; tumour; pancreatic disorder; cirrhosis pancreatitis; thyroiditis; goiter; Graves' disease; gastric disorder; gastritis; tumour; placental disorder; placentitis; spontameous abortion pulmonary disorder; aclectasis; edema; Goodpasturc's syndrome: muscular dystrophy; cardiovascular disorder; ischemic heart disease; congenital heart disease; cerebral edema; cerebrovascular disease; hepatic disorder; jaundice; hepatitis; jeukocytic disorder; hyperplasia; leukopenia; leukocytosis; malignant lymphoma; prostate disorder;
                                                                                                                                  TANGO 201: TANGO 223; secreted protein; transmembrane protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "protein kinase C phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'note- "casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                      "casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19. 41
/noter "protein kinase C phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /noter "casein kinase II phosphorylation site"
115..117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "protein kinase C phosphorylation site"
122..125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "casein kinase II phosphorylation site"
169..172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "protein kinase C phosphorylation site'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "casein kinase II phosphorylation site'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note- "extraceilular domain"
/note- "extraceilular domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "N-glycosylation site"
197..202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note- "N-glycosylation site"
124..126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          140..143
/note= "N-glycosylation site"
157..160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "N-glycosylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "N-glycosylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "transmembrane domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "N-glycosylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "myristoylation site"
216..238
                                                                                                                                                                                                                                                                                                                                                                                                                                                       "myristoylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "cytoplasmic domain"
                                                                                                                                                                                                                                                                                                                                                                                   /note= "signal peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "mature protein"
                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
1..29
 Š
 AAB08541 standard; Protein; 247
                                                                                                 A human TANGO 223 polypeptide.
                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "N
179..182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "t
226..229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "c.
239..247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note- "p
134..137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "N
159..161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ..110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ..162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30..247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          97..90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note-
                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'note≖
                                                                                                                                                                                                                                                                                                                                                                                                                      /note-
                                                                                                                                                                                                                                                                                       inflammatory disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                W0200050442-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                        Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                        Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Adified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Modified-site
                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                  02-JAN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31-AUG-2000
                                  AAB08641;
                                                                                                                                                                                                                                                                                                                                                                       Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ucmain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Domain
 ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention relates to novel human GENSET coding sequences (ACC51050-ACC51115) and proteins (ABR48453-ABR48508). The GENSET sequences are useful for preparing a composition for treating GENSET-related disorders. They can also be used as markers for tissues in which the corresponding protein is preferentially expressed, as molecular weight markers on Southern gels, as chromosome markers or tags to identify chromosomes, and as reagents in assays to quantitatively determined levels of GENSET expression in biological samples.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               135 CTNYTA--HVSC----FPAPNITCKDSSGNETHFTGNEVGFFKPISCRNVNGYSYKVAVA 188
 112 CINSTSCMTVSCPRORYPA-NCTVRD----HVHCLGNRT-FPKMLYCNWTGGYKWSTALA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              189 LSLFLGWLGADRFYLGYPALGLLKFCTVGFGG:GSLIDFILISMQIVGPSDGSSY: 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LSLFLGWLGADRFYLGYPALGLLKFCTVGFCGIGSLIDFILISMQ1VGPSDGSSYI 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New GENSET polynucleotides and polypeptides, useful for preparing a composition for treating GENSET related disorders and as reagents in assays to quantitatively determined levels of GENSET expression in blobogical samples
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 221;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ouery Match 13.9%; Score 200; DB 24; Length 2: Best Local Similarity 45.7%; Pred. No. 2.4e-12; Matches 53; Conservative 12; Mismatches 39; Indels
                                                                                                                                                                                                                                                                     Human Amyloid Apoptotic Receptor (AAR) protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 2; Page 475-476; 505pp; English.
                                                                                                                                                                                                                                                                                                      Human; GENSET; therapeutic; therapy
-
-
-
::
                                                                                                                                                                     Ą
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-JUN-2001; 2001US-298698P.
29-JUN-2001; 2001US-302277P.
13-JUL-2001; 2001US-305456P.
                                                                                                                                                                    ABR48493 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                      06-AUG-2001; 2001WO-IB01715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25-MAY-2001; 2001US-293574P.
                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bejanin S, Tanaka H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2003-129412/12.
N-PSDB; ACC51160.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           221 AA;
                                                                                                                                                                                                                                                                                                                                                                     WO200294864-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (GEST ) GENSET
                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                    13-JUN-2003
                                                                                                                                                                                                                                                                                                                                                                                                      28-NOV-2002
                                                  189
                                                                                                                                                                                                     ABR48493;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 14
AAB08641
                                                                                                                                                  ABR48493
```

a

ò

us-09-852-100a-2.raq

Sat

6

```
3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ú.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  135 CINYTA--HVSC----FPAPNIICKDSSGNETHFIGNEVGFFFFFISCRNVNGYSYKVAVA (8)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TANGO 201; TANGO 223; secreted protein; transmembrane protein; proliferative disorder; neoplasm; tumour; pancreatic disorder; cirrhosis; pancreatitis; typyrolditis; goiter; Graves' disease; gastric disorder; gastritis; tumour; placental disorder; placentitis; spontaneous abortion; pulmonary disorder; atelectasis; edema; Goodpasture's syndrome; muscular dystrophy; cardiovascular disorder; ischemic heart disease; congenital heart disease; cerebral edema; cerebrovascular disease; hepatic disorder; jaundice; hepatitis; leukocytic disorder; hyperplasia; leukopenia; leukocytosis; malignant lymphoma; prostate disorder; inflammatory disease.
                                                                                                                                                                                                                                                                                                              The present sequence represents TANGO 223 polypoptide. The specification also describes a TANGO 201 polypeptide. These polypeptides are secreted or transmembrane proteins. Human TANGO 201 and 223 nucleic acids, proteins and their modulators are useful for treating proliferative disorders e.g. neoplasms or tumours, pancreatic disorders (e.g. pancreatitis), disorders of the adrenal cortex, adrenal medulia, thyroid gland (e.g. thyroiditis), goiter, Graves' disease, gastric placenteit of astrictis or tumours), placenteid disorders (e.g. pastrictis or tumours), placenteid disorders (e.g. pattendancous abortion), pulmonary disorders (e.g. attendancous abortion) attendancous abortion).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    brain (e.g. cerebral edema), cerebrovascular disease and to treat injury or trauma to the brain. They are also useful for treating hepatic disorders (e.g. jaundice, hepatitis, cirrhosis or malignant tumours), renal, testicular, intestinal disorders. TNGO 23 polynouclectides are also useful for treating lenkocytic disorders (e.g. leukocytosis and malignant lymphomas) and prostate disorders (e.g. inflammatory diseases, hyperplasia or tumours).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 muscle (e.g. muscular dystrophy), cardiovascular disorders (e.g. ischemic heart disease and congenital heart disease), disorders of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           138 CINSTSCMTVSCPRORYPA-NCTVRD----HVHCLONRT-FPKMLYCNWTGGYKWSTALA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         189 LSLFLGWLGADRFYLGYPALGLLKFCTVGFCGIGSLIDFILJSKGIVGPSDGSSY: 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12; Gaps
                                                                                                                                                                                                    Novel nucleic acid molecule encoding secreted or transmembrane prouseful for identifying modulators and for diagnosing and treating pancreatic, cardiovascular, liver and pituitary disorders -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Match 13.9%; Score 200; DB 21; Length 247; Local Similarity 45.7%; Pred. No. 2.8e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A human TANGO 223 variant polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB08656 standard; Protein; 247 AA
                                                                                                                                                                                                                                                                           Claim 9; Fig 8; 176pp; English.
                                                                           (MILL-) MILLENNIUM PHARM INC
25-FEB-2000; 2000WO-US04784.
                                      990S-0259388
                                                                                                                                                                   N-PSDB; AAA64408, AAA64409.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               53; Conservative
                                                                                                                                                  WPI; 2000-572066/53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      247 AA;
                                    26-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               02-JAN-2001
                                                                                                               McCarthy SA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sednence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ouery Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB08656;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB08656
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    õ
```

```
135 CTNYTA--HVSC----FPAPNITCKDSSGNETHFTGNEVGFFKPISCRNVNGYSYKVAVA 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence represents a TANGO 223 variant. The specification also describes a TANGO 201 polypeptide. These polypeptides are secreted or transmembrane proteins. Human TANGO 201 and 223 nucleic acids,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     brain (e.g. cerebral edema), cerebrovascular disease and to treat injury or trauma to the brain. They are also useful for treating hepatic disorders (e.g. jaundice, hepaticis, cirrhosis or malignant tumours), renal, testicular, intestinal disorders. TANGO 223 pclynucleotides are also useful for treating leukocytic disorders (e.g. leukopenias, leukocytosis and malignant lymphomas) and prostate disorders (e.g. inflammatory diseases, hyperplasia or tumours).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel nucleic acid molecule encoding secreted or transmembrane protein useful for identifying modulators and for diagnosing and treating pancreatic, cardiovascular, liver and pituitary disorders -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              disorders e.g. neoplasms or tumours, pancreatic disorders (e.g. pancreatitis), disorders of the adrenal cortex, adrenal medulla, thyroiditis), goiter, Graves' disease, gastric disorders (e.g. gastrits or tumours), placental disorders (e.g. placentitis or tumours), placental disorders (e.g. placentitis or spontaneous abortion), pulmonary disorders (e.g. placentitis or spontaneous abortion), pulmonary disorders (e.g. muscular dystrophy), cardiovascular disorders (e.g. ischemic heart disease and congenital heart disease), disorders of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            189 LSLFLGWLGADRFYLGYPALGLLKFCTVGFCGIGSLIDFILLISMQIVGPSDGSSYI 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                proteins and their modulators are useful for treating proliferative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           39; Indels 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 247;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Obery Match
Best Local Similarity 45.7%; Pred. No. 2.8e-12;
Matches 53; Conservative 12; Mismatches 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Search completed: September 26, 2003, 17:25:14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 9; Page 169-170; 176pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                       (MILL-) MILLENNIUM PHARM INC
                                                                                                                                                                                                                                                                                                                     99US-0259388
                                                                                                                                                                                                                                        25-FEB-2000; 2000WO-US04784
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI: 2000-572066/53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            247 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; AAA64424.
                                                                         W0200050442-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Job time : 89 secs
                                                                                                                                                                                                                                                                                                                          26-FEB-1999;
HOMEO Sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         McCarthy SA;
                                                                                                                                                          31-AUG-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
```

ŝ

		:

Н

```
Query Match
Best Local Similarity 27.7%
Matches 36; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            609-520-3259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SS: single
linear
amino acid
                                                                                                                                                                                                                                                                                                                                                   USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                          08543
                                                                                                                                                                                                                                                                                                                                            Ż
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-414-657D-45
                                                                                                                                                                                                             US-08-414-657D-45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                          STATE: N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX:
16958; A
44, Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                       4253, Ap
2, Appli
2, Appli
2, Appli
2, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Appli
Appli
Appli
Appli
Appli
Appli
                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 43, Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Appli
Appli
Appli
Appli
Appli
Appli
Appli
                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 45, Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                4, Appl
                                                                    (without alignments)
379.387 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                        Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                       Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
Sequence
Sequence
Sequence
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                           : Search time 30 Seconds
                                                                                           US-09-852-100A-2
1439
1 MHILKGSPNVIPRAHGQKNI.....TRLTRLSITNETFRKTGLYP
                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                              /cgn2_6/ptodata/l/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/l/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/l/iaa/fb_COMB.pep:*
/cgn2_6/ptodata/l/iaa/backfilesl.pep:*
       GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                              /cgn2_6/ptodata/1/iaa/5A_COMB.pcp:*/cgn2_6/ptodata/1/iaa/5B_COMB.pcp:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-252-991A-16958
US-08-414-6570-44
US-08-414-6570-2
US-08-135-080-2
US-09-135-080-2
US-09-611-781-4
US-08-611-781-4
US-08-611-781-4
US-08-611-781-4
US-08-850-917-2
US-08-850-917-2
                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-135-080-4
US-09-328-352-4253
US-08-177-109A-2
US-08-177-109A-2
US-09-182-728A-2
US-09-795-232-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-328-352-7922
US-08-700-013B-19
                                                                                                                                                                                                                                                                                                                                                                                                             -08-414-657D-42
-08-414-657D-43
                                                                                                                                                                                                                                                                                                                                                                                                      US-08-414-657D-45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -08-700-013B-9
-08-700-013B-21
                                                                                                                                                                         Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5-09-181-706-8
5-09-458-791-8
5-09-459-066-8
5-09-459-065-8
                                                                                                                                                         328717 seqs, 42310858 residues
                                                                                                                                                                                                                                                                                                                                                           SUMMARIES
                                                          September 26, 2003, 17:25:22
                                                                                                                                                                                                                   Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                         - protein search, using sw mode.
                                                                                                                                       Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                       Issued_Patents_AA:*
                                                                                                                                                                                           seq length: 0 seq length: 2000306000
                                                                                                                                                                                                                                                                                                                                                                                     Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     456
1237
328
328
660
660
660
927
797
                                                                                                                                BLOSUM62
                                                                                                                                                                                                                                                                                                                                                                             Query
                                                                                                                                                                                                                                                                                                                                                                                                     σασασασοροροροσοροσοσοικικο
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 79.5
79.5
79.5
                                                                                             Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                     Score
                                                                                                                               Scoring table:
                                                                                                                                                                                           Minimum DB
Maximum DB
                                           OM protein
                                                                                                              sednence:
                                                                                                                                                         Searched:
                                                                                                                                                                                                                                                       Database
                                                           Run on:
                                                                                                                                                                                                                                                                                                                                                                             Result
No.
```

```
sequence 26323, A
sequence 2, Appli
Sequence 2, Appli
Sequence 21426, A
Sequence 3, Appli
Sequence 3, Appli
                                          Sequence 6, Appli
Sequence 2, Appli
Sequence 31718, A
Sequence 120, App
Sequence 122, App
Sequence 4, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
Sequence
                        Sequence
                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5.9%; Score 85; DB 2; Length 310; 27.7%; Pred. No. 1.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Parcnt No. 5861283
GENERAL INFORMATION:
APPLICANT: Pimenta, Aurea
APPLICANT: Fischer, Itahak
APPLICANT: Pimenta, Victoria
APPLICANT: Pimenta, Victoria
TILLE OF INVENTION: Limble System-Associated Membrane
TILLE OF INVENTION: Limble System-Associated Membrane
NUMBER OF SQUENCES: 60
CORRESPONDENCE ADDRESS:
             US-08-414-6570-60
US-09-135-080-8
US-09-112-498-72
US-09-1252-991A-26135
US-09-252-991A-26135
US-09-191-468-122
US-09-191-468-122
US-09-191-468-122
US-09-191-468-122
US-09-252-991A-26323
US-09-252-991A-26323
US-08-356-340-2
US-08-356-340-2
US-08-356-340-2
US-08-356-340-2
US-08-36-685-5
US-09-150-460B-11
US-08-836-68B-37
US-08-836-68B-37
US-08-836-68B-37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Dechert Price & Rhoads
STREET: 997 Lenox Drive, Building 3, Suite 210
CIIY: Lawrenceville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           47;
US-09-252-991A-19777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MADIUM TYPE: Diskette
COMPUTER: IBM Compatible
COMPATING SYSTEM: DOS
SOFTWARE: FastSEC for Windows Version 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                            ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/414.657D
FILING DATE: 31-MAR-1995
CLASSIFICATION 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 317743-162 FELECOMMUNICATION INFORMATION: TELEPHONE: 609-520-3214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Seguence 45, Application US/08414657D
Patent No. 5861283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Bloom, Allen
REGISTRATION NUMBER: 29,135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 310 amino acids
```

~

g ò a οÿ

```
: | : |||| | | :: | | :|| | :: | | :|| | | :: | | :| | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | :: | | :: | :: | | :: | :: | | :: | :: | | :: | :: | | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             101 SAGGEESLKCEDLKVG----QYICKDPKINDATQEPVNCTNYTAHVSCFPAPNITCKDSS 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  157 GNETHFIGNEVG-----FFKPISCRNVNGYSYKVAVALSLFLGWLGADRFYLGYPALG 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 5.9%; Score 85; DB 2; Length 338; Best Local Similarity 27.7%; Pred. No. 2; Matches 36; Conservative 15; Mismatches 47; Indels
                                                                                                                                                                                                                                                                                                                         APPLICANT: Levit, Pat
APPLICANT: Levit, Pat
APPLICANT: Finenta, Aurea
APPLICANT: Fischer, Itzhak
APPLICANT: Fischer, Victoria
TITLE OF INVENTION: Limbic System Associated Membrane
TITLE OF INVENTION: Limbic System Associated Membrane
NYMER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AUDRESSEE: Dechert Price & Rhoads SIRRET: 997 Lenox Drive, Building 3, Suite 210 CITY: Lawrenceville SIARE: NJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: FASTSEQ for Windows Version 2.0 CURRENT APPLICATION DAIA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             317743-102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                JANER: US/08/414,657D
                                                                                                                                                                                                                                  Sequence 43, Application US/08414657D Patent No. 5861283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 4, Application US/09135080; Patent No. 6423827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Bloom, Allen
REGISTRATION NUMBER: 29,135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 31
TELECOMMUNICATION INFORMATION:
TELEPHONE: 609-520-3214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM Compatible OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Bloom, Allen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ 1D NO: A SEQUENCE CHARACTERISTICS: LENGTH: 338 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 609-520-3259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      210 LLKFCTVGFC 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     329 ASLFCLLSKC 338
210 LLKFCTVGFC 219
                                                                  329 ASLFCLLSKC 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
SIRANDEDNESS: Sir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
                                                                                                                                                                                                                                                                     Patent No. 5861283
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      08543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-414-657D-43
                                                                                                                                                                                                   US-08-414-657D-43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-135-080-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 4
                                                                                                                                                                       RESULT 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ŝ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ::
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5
      8
                                                           G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  101 SAGGEESLKCEDLKVG----QYICKDPKINDATQEPVNCTNYTAHVSCFPAPNITCKDSS 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 230 TTGROASLKCEASAVPAPDFEWYRDDTRINSANGLEIKSTE---GOSSLTVTNVT-EEHY 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   157 GNETHFTGNEVG-----FFKP1SCRNVNGYSYKVAVALSLFLGWLGADRFYLGYPALG 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GNYTCVAANKLGVTNASLVLFRPGSVRGING-SISLAVPL-----WL-----LA 300
                                  101 SAGGEESLKCEDLKVG----QYICKDPKINDATQEPVNCTNYTAHVSCFPAPNITCKDSS 156
                                                                                                                                                                   157 GNETHFTGNEVG------FFKPISCRNVNGYSYKVAVALSLFLGWLGADRFYLGYPALG 203
                                                                                                 202 TTGRQASLKCEASAVPAPDFEWYRDDTRINSANGLEIKSTE---GOSSLTVTNVT-FERY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5.9%; Score 85; DB 2; Length 338; 27.7%; Pred. No. 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   47; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Pimenta, Aurea
APPLICANT: Fischer, Itzhak
APPLICANT: Shukareva, Victoria
TITLE OF INVENTION: Limbic System-Associated Mcmbrane
NUMBER OF SEQUENCES: 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   E: Dechert Price & Rhoads
997 Lenox Drive, Building 3, Suite 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM: 00S
SOFTWARE: FASISED for Windows Version 2.3
SOFTWARE: FASISED for Windows Version 2.3
APPLICATION LOAD
FILING DATE: 31-MAR-1995
CLASSIFICATION: 435
APPLICATION NUMBER:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Bloom, Allen
REGISTATION NUMBER: 29,135
REFERENCE/DOCKET NUMBER: 317743-102
TELECOMMUNICATION INFORMATION:
TELEPHONE: 609-520-3214
TELEFAX: 609-520-3259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 42, Application US/08414657D Patent No. 5861283 GENERAL INFORMATION: APPLICANT: Levitt, Pat APPLICANT: Pimenta, Aurea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               42:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 338 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                36; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         single
                                                                                                                                                                                                                                                                                                                                                                   301 ASLFCLLSKC 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS: ADDRESSER: Dechert P
                                                                                                                                                                                                                                                                                                 210 LLKFCTVGFC 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 99/ Leurarty: Lawrenceville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
Matches 36; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           08543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-414-657D-42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-414-657D-42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                               258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
```

7 ;

ò

```
12;
                                                                                                                                                                                                                        78 TARLVGVL---WFVSVTTGPW-----GAVATSAGGEESLKCEDLKV------G 136
                                                                                                                                                                                                                                                                     57 ITGLYGPLNVEWITRLERGPYWSEKIDEKGTFFRGAPGSISIRSPDYPSIPGQPAAIDGG 116
                                                                                                                                                                                                                                                                                                                    117 QYICKDPKINDATQEPVNCTNY - - TAHVSC - FPAPNITCKDSSGNETHFTGNEVGFFKPI 173
                                                                                                                                                                                                                                                                                                                                               174 SCRNVNGYSYKVAVALSLFLGWLGADRFYLGYPALGILKFCTVGFCGIGSLIDFILLISMQ 2:3
                                                                                                                                                                                                                                                                                                                                                                                                                                                               159 ASHKVSLVSFATAGTVGGVTGAIIGKNFSSGNMSYGQATGAGAAGGAIGGLIVAAIINAE 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                           52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62;
                                                                                                                       5.8%; Score 84; DB 4; Length 258; 23.5%; Pred. No. 1.7; ative 24; Mismatches 93; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 764;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   71; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              234 ---IVG--PSDGSSYIIDYYGTRLTRLSITNETFRKIQLYP 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           219 VGKIIGGLPIKESSFM----EKLRELGAKREPLKQISLLP 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Dennis E. Hourcade and Teresa J. Oglesby
TITLE OF INVENTION: MODIFIED COMPLEMENT PROTEASES
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
ADDRESSEE: Patrea L. Pabst
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTMANE: Statent N. CONT. STATEMENT APPLICATION DATA TO CURRENT APPLICATION DATA TO STATEMENT APPLICATION NUMBER: 03.74N-1994
CLASSIFICATION: 514
ATTCKNEY/AGENT INFORMATION: NAME: Pabbit, Patrea L. REGISTRATION NUMBER: 1, 284
REGISTRATION NUMBER: 1, 284
REGISTRATION NUMBER: 1, 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 5.8%; Score 83; DB 2; Best Local Similarity 24.1%; Pred. No. 10; Matches 49; Conservative 21; Mismatches 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Patrea L. Pabst
STREET: 2800 One Atlantic Center
STREET: 1201 West Peachtree Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24 GTGLYPMRGPFKNLALLPFSLPLLGGG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2, Application US/08177109A
Patent No. 5869615
                                                    ORGANISM: Acinetobacter baumannii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: WL
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (404) 873-8794
TELEFAX: (404) 873-8795
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                               Stery Match
Hest Local Similarity 23.5%
Watches 52; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGIH: 764 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 30309-3450
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Atlanta
STATE: Georgia
CCUNTRY: USA
                                                                          US-09-328-352-4253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 6
US-08-177-109A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-177-109A-2
    LENGTH: 258
                             TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                               <u>a</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ð
                                                                                                                                                                                                                          ð
                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                    ੋਂ
                                                                                                                                                                                                                                                                                                                                                                 9
                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
APPLICANT: Gary L. Breton et al.
IITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEGUENCES RELATING TO ACINETORACTER
IITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERBNCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT PILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 4253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              101 SAGGEBSLKGEDLKVG----QYICKDPKINDATQEPVNCTNYTAHVSCPPAPNITCKUSS 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        230 TTGRQASIKCEASAVPAPDFEWYRDDIRINSANGLEIKSIE---GUSSLIVINVI-EEHY 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        157 GNETHFTGNEVG-----FFKPISCRNVNGYSYKVAVALSLFIGWLGADRFYLGYPALG 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 4; Length 338;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                          APPLICANT: Pimenta, Aurea
APPLICANT: Fischer, Itzhak
APPLICANT: Fischer, Itzhak
ITZHE OF INVENTION: Limble System-Associated Membrane
TITLE OF INVENTION: Protein and DNA
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                SEE: Dechert Price & Rhoads: 997 Lenox Drive, Building 3, Suite 210 Lawrenceville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7.7
                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM: DOS
SOFTWARR: FastSOG for Windows Version 2.0
SURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/135,080
FILING DATE: 17-AGG-1998
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ouery Match 5.9%; Score 85; DB 4;
Best Local Similarity 27.7%; Pred, No. 2;
Matches 36; Conservative 15; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          317743-102A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 4253, Application US/09328352 Patent No. 6562958
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 08/414,657
FILING DATE: 31-MAR-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Bloom, Allen
REGISTRATION NUMBER: 29,135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 31
TELECOMMUNICATION INFORMATION:
TELEPHONE: 609-620-3214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 4: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                       S: Diskette
IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGIH: 338 amino acids
TYPE: amino acid
STRANDEDNESS: single
                             Levitt, Pat R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 609-620-3259
                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21C LLKFCTVGFC 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     329 ASLFCLLSKC 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                 USA
                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM IYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 5
US-09-328-352-4253
                                                                                                                                                                                                                                                                                                                                     08543
                                                                                                                                                                                                                   ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TOPOLOGY:
US-09-135-080-4
                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                            STREET:
```

g ò ò

```
87 FVSVTTGPWGAVATSAGGEESLKCED---LKVGQYICKD-PKINDATQEPVNCTNYTAHV 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 199 DREYLGYPAL-----GLLKFCTVGFCGIGSLIDFILISMQIVGPSDGSSYIIDXYGTR 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           143 SCFPAPNITCKESSGNETHFTGNEVGFFKPISCRNVNGYSY----KVAVALSLFJGWLGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     349 TAYPNVTMVNFTSQANKTFVSGSE-EYFKYFVLKISAGIEYPGEIRWPLALCLFLAWV--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5.6%; Score 81; DB 3; Length 797; 23.9%; Pred. No. 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        80:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    32; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Anthony M. Brown
APPLICANT: Conrad Gerald Chapman
APPLICANT: Statel Simon Gloger
APPLICANT: Joanne Rachel Evans
APPLICANT: Joanne Rachel Evans
APPLICANT: William Cairns
APPLICANT: Hugh Jonathan Herdon
TITLE OF INVENTION: NOVEL COMPOUNDS
FILE REFERENCE: GP-30176-D1
CURRENT APPLICATION NUMBER: US/09/795,232
CURRENT FILING DATE: 2001-02-28
PRIOR APPLICATION NUMBER: 1998-10-29
PRIOR PELICATION NUMBER: 9818890.7
PRIOR FILING DATE: 1998-08-28
                                                                                                                                                                                                                                                                                                                                                                                                         FILE REFERENCE: GP-30176
CURRENT APPLICATION NUMBER: US/09/182,728A
CURRENT FILING DATE: 1998-10-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                    APPLICANT: BROWN, ANTHONY
APPLICANT: CHAPMAN, CONRAD GERALD
APPLICANT: GLOGER, ISRAEL SIMON
APPLICANT: EVANS, JOANNE RACHEL
APPLICANT: CATRNS, WILLIAM
APPLICANT: HERDON, HUGH
                                                             167 VGFFK----PISCRNVNGYSYKV 185
                                                                                                162 AGYCSNPGIPIGTRKV-GSQYRL 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: 9818896.7
PRIOR FILING DATE: 1998-10-29
PRIOR FILING DATE: 1998-08-28
SOUTWARE: FEATURE ID NOS: 6
                                                                                                                                                                                                           Sequence 2, Application US/09182728A Patent No. 6238883
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2, Application US/09795232 Patent No. 6426405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  252 LIRLSITNEIFRKTOLY 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       461 LINATVWKDA--ATOIF 475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Clery Match
Hest Local Similarity 23.9%
Watches 47, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: HOMO SAPIENS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER
SOFTWARE: FAST
SEQ ID NO 2
                                                                                                                                                                                       CS-09-182-728A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-182-728A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-795-232-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ô
                                                               ें
                                                                                                    q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ें
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 SKMAAAWPSG--PSAPEAVTARLVGVLWFVSVTTGPWGAVATS-----AGGEESLKC-- 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            56 QALEYVCPSGFYPYPVQTRTCR-----STGSKSTLKTQDQKIVRKAECHAIECPR 195
                                           61 SKMAAAWFSG--PSAPEAVTARLVGVLWFVSVTTGPWGAVATS-----AGSEESLKC-- 110
                                                                                OALEYVCPSGFYPYPVQTRTCR----STGSWSTLKTQDDQKTVRKAECRAIHCFR 165
                                                                                                                          -EDLKVGQYICKDPKINDAIQEPVNC-INYTAHVSCFPAPNITCKDSS--GNETHFIGNE 166
                                                                                                                                                      111 -EDLKVGQYICKDPKINDATQEPVNC-TNYTAHVSCFFAPNITCKDSS--GNETHFTGNE 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 GSNLSP-----QLCLMPFILGLLSGGVTTTPWSLAQPQCSCSLEGVEIKGGSFRLLQEG 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sabs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 2; Length 764;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      71: Indels
                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Dennis E. Hourcade and Teresa J. 04:esby
TITLE OF INVENTION: MCDIFIED COMPLEMENT PROTEASES
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/687,706
FILING DATE: 26.7UL-1996
CLASSIPICATION: 514
PRIOR APPLICATION DATA:
APPLICATION UMBER: US 08/177,109
FILING DATE: 03.JAN-1994
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5.8%; Score 83; DB 24.1%; Pred. No. 10; tive 21; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: WU 107 DIV
TELECOMUNICATION INFORMATION:
TELEFAR: (404) 873-8794
INFORMATION FOR SEQ 10 NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 764 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24 GIGLYPMRGPFKNLALLPFSLPLLGGG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Patrea L. Pabst
STREET: 2800 One Atlantic Center
STREET: 1201 West Peachtree Street
                                                                                                                                                                                                                                       :: 11 | | | ::
162 AGYCSNPGIPIGTRKV-GSQYRL 183
                                                                                                                                                                                                             167 VGFFK----PISCRNVNGYSYKV 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      s: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                       Sequence 2, Application US/08687705
Patent No. 5928892
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   : 764 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 24.18
Matches 49; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30309-3450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 1201 We
CITY: Atlanta
STATE: Georgia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Georgia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                     US-08-687-706-2
                                                                                                                                                                                                                                                                                                                    RESULT 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QQ
                                                                                qq
                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                           ò
                                                                                                                            ò
                                                                                                                                                                 qq
```

S

```
101 SAGGEESLKCEDLKVG----QYICKDPKINDATQEPVNCTNYTAHVSCFPAPNIICKDSS 1:6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  202 TTGRQASLKCEASAVPAPDFEWYRDDTRINSANGLEIKSTE---GQSSLIVTNVT-EEHY 25.7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          258 GNYTCVAANKLGVINASLVLFRPGSVRGING-S1SLAVPL----WL 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  157 GNETHFTGNEVG-----FFKPISCRNVNGYSYKVAVALSLFLGWL 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 304;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Levitt, Pat
APPLICANT: Planenta, Aurea
APPLICANT: Planenta, Aurea
APPLICANT: Placher, Ithak
APPLICANT: Tischer, Ithak
APPLICANT: Zhukareva, Victoria
TITLE OF INVENTION: Limbic System-Associated Membrane
NUMBER OF SEQUENCES: 60
                        : 997 Lenox Drive, Building 3, Suite 210 Lawrenceville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E: Dechert Price & Rhoads
997 Lenox Drive, Building 3, Suite 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 2;
                                                                                                                                                                                COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOCHWARE: FastSED for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/414.657D
FILING DATE: 31-MAR-1995
CLASSIPICATION: 435
PRIOR APPLICATION 435
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SYSTEM: DOS
FastSEQ for Windows Version 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match 5.6%; Score 80.5; D Best Local Similarity 29.9%; Pred. No. 4.8; Matches 32; Conservative 14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              317743-102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/414,657D
       Dechert Price & Rhoads
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2, Application US/08414657D Patent No. 5861283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REGISTRATION NUMBER: 29,135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION: TELEPHONE: 609-520-3214
                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION: NAME: Bloom, Allen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 304 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO:
                                                                                                                                                                      Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 609-520-3259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SS: single
linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
                                                                                                                   2IP: 08543
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lawrenceville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                              USA
                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 08543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            : TOPOLOGY:
US-08-414-657D-44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 12
US-08-414-657D-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ç,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ें
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: MARC J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING ID PSECECHONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT PILING DATE: 1999-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
                                                                                                                                                                                                                                     :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  349 TAYPNVIMVNFTSQANKTFVSGSE-EYFKYFVLKISAGIEYPGEIRWPLALCLFLAWV-- 405
                                                                                                                                                                                                                                                                              87 FVSVTTGPWGAVAISAGGEESLKCED----LKVGQYICKD-PKINDATQEPVNCTNYTAHV 142
                                                                                                                                                                                                                                                                                                                         302 PVSVL--PWGSCNNPWNTPE---CKDKTKLLLDSCVISDHPKI------GIKNSTFCN 348
                                                                                                                                                                                                                                                                                                                                                                       143 SCFPAPNITCKDSSGNETHFIGNEVGFFKPISCRNVNGYSY----KVAVALSLFLGWLGA 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     199 DRFYLGYPAL-----GLLKFCTVGFCGIGSLIDFILISMQIVGPSDGSSYIIDYYGTR 251
                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                     38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 181 YSYKVAVALSLFLGWLGADRFYLGYPALGLLKFCTVGFCGIGSLIDFIL: 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5.6%; Score 80.5; DB 4; Length 150; 40.0%; Pred. No. 1.8; Live 7; Mismatches 22; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 44, Application US/08414657D
Patent No. 5861283
GENERAL INFORMATION:
APPLICANT: Levitt, Pat
APPLICANT: Fischer, Itzhak
TITLE OF INVENTION: Limbic System-Associated Membrane
TITLE OF INVENTION: Limbic System-Associated Membrane
TITLE OF INVENTION: Limbic System-Associated Membrane
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                     5.6%; Score 81; DB 4; Length 797, 23.9%; Pred. No. 17;
                                                                                                                                                                                  Ouery Match 5.6%; Score 81; DB 4; Length 1978 Best Local Similarity 23.9%; Pred. No. 17; Matches 47; Conservative 32; Mismatches 80; Indels
  SEQ ID NOS: 6
FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-252-991A-16958
; Sequence 16958, Application US/09252991A
; Patent No. 6551795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          461 LINATVWKDA--ATOIF 475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            252 LTRLSIINETFRKTQLY 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                         TYPE: PRT
ORGANISM: HOMO SAPIENS
NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 20; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-252-991A-16958
    SOFTWARE: Fast
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO 16958
LENGTH: 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-414-657D-44
                                                                                                                                       US-09-795-232-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 11
                                                                                                                                                                                                                                                                                                                         C<sub>C</sub>
                                                                                                                                                                                                                                                                                                                                                                                                            Ωp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               q
                                                                                                                                                                                                                                                                                                                                                                       5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
```

Gaps

ø

```
101 SAGGEESLKCEDLKVG----QYICKDPKINDATQEPVNCTNYTAHVSCFPAPNITCKDSS 156
                                                                                                                                                                                                                                                                                                                                                   223 TTGRQASLKCEASAVPAPDFEWYRDDTRINSANGLEIKSTE---GQSSLTVTNVT-EEHY 278
                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                               21;
                                                                                                                                                                                                                                                                                                                                                                                                                     279 GNYTCVAANKLGVINASLVLFRPGSVRGING-SISLAVPL----WL 319
                                                                                                                                                                                                                      Length 325;
                                                                                                                                                                                                                                                                                                                                                                                              157 GNEIHFTGNEVG-----FFKPISCRNVNGYSYKVAVALSLFLGWL 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5.6%; Score 80.5; DB 4; Length 325;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2, Application US/09135080
Patent No. 6423827
GENERAL INFORMATION:
APPLICANT: Levitt, Pat R.
APPLICANT: Fischer, Itzhak
APPLICANT: Zhukareva, Vitcoria
TITLE OF INVENTION: Limbic System-Associated Membrane
TITLE OF INVENTION: Protein and DNA
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: ADDRESSE: ADDRESSE:
ADDRESSEE: Dechert Price & Rhoads
STREET: 997 Lenox Drive, Building 3, Suite 210
                                                                                                                                                                                                                                                               14; Mismatches 40; Indels
                                                                                                                                                                                                                   Score 80.5; DB 2;
Pred. No. 5.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUFFWARE: FASTSED for Windows Version 2.0 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/no....
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOWNER TOWN Aller HEGISTRATION NUMBER: 29,135
REGISTRATION NUMBER: 317743-102A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17-Aug-1998
N: 11-Aug-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/414,657
FILING DATE: 31-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Bloom, Alle:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 31
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                   Query Match
Best Local Similarity 29.9%;
Matches 32; Conservative 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ 1D NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 325 amino acids TYPE: amino acid
                                         INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
LENGTH: 325 amino acids
IYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            609-620-3214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 609-620-3259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein FRAGMENT TYPE: internal
  TELEFAX: 609-520-3259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 997 Lenox Dr
CITY: Lawrenceville
STAIE: NJ
COUNTRY: USA
                                                                                                                                                        TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 17 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             08543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE:
                                                                                                                                                                          US-08-414-657D-41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 14
US-09-135-080-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-135-080-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cuery Match
                                                                                                                                                                                                                                                                                                                                                   9
                                                                                                                                                                                                                                                                                                                                                                                                 ें
                                                                                                                                                                                                                                                                                                                                                                                                                                     ۲
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         101 SAGGEESLKCEDLKVG----QYICKDPKINDATQEPVNCTNYTAHVSCFFAPNITCKDSS 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  223 TIGROASLKCEASAVPAPDFEWYRDDTRINSANGLEIKSTE---GOSSLIVINVI-FEHY 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           279 GNYICVAANKLGVTNASLVLFRPGSVRGING-SISLAVPL----WL 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ouery Match 5.6%; Score 80.5; DB 2; Length 325; Best Local Similarity 29.9%; Pred. No. 5.3; Matches 32; Conservative i4; Mismatches 46; Indels 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              157 GNETHFTGNEVG-----FFKPISCRNVNGYSYKVAVALSLFIGWI. 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Levitt. Pat
APPLICANT: Fischer, Austa
APPLICANT: Fischer, Itahak
APPLICANT: Fischer, Itahak
APPLICANT: Lukareva, Victoria
TITLE OF INVENTION: Limbic System-Associated Membranc
TITLE OF INVENTION: Limbic System-Associated Membranc
TITLE OF INVENTION: Protein and DNA
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dechert Price & Rhoads
STREET: 997 Lenox Drive, Building 3, Suite 210
CITY: Lawrenceville
STATE: NJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: FastSEO for Windows Version 2.0 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/414,657D
FILING DATE: 31-MR-1995
CLASSIFICATION: 435
PRIOR APPLICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29,135
SER: 317743-102
                                                                                                                           NAME: Bloom, Allen
REGISTRATION NUMBER: 29,135
REPERCELOCKET NUMBER: 317743-102
TELECOMMUNICATION INCHMENTION:
TELECHONE: 609-520-3214
TELEFAX: 609-520-3259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 41, Application US/08414657D Patent No. 5861283 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER: 29,135
REFERENCE/COCKET NUMBER: 31
TELECOMMUNICATION INFORMATION:
TELEPHONE: 609-3214
FILING DATE: 31-MAR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
                                                                                                        ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 325 amino acid
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein
FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                        single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                    CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bloom, Allen
                                                                                                                                                                                                                                                                                                                                                                                                 linear
                                                                                                                                                                                                                                                                                                                                                   TYPE: amino a STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            08543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 13
US-08-414-657D-41
                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: N. COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-414-657D-2
```

qo ò

```
ŝ
                                                                                 3
                                                                                                                            5
                                                                                                                                                                   3
                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Belt, Judith A.
APPLICANT: Crawford, Charles R.
APPLICANT: Crawford, Charles R.
APPLICANT: Patel, Divyen
IIILE OF INVENTION: A NITROBENZYLMERCAPTOPUNINERIBUSIDE
IIILE OF INVENTION: (NBMPR)-INSENSITIVE, EQUILIBRATIVE, NUCLEUGIEDE IRANSPORT
ITILE OF INVENTION: PROTEIN, NUCLEIC ACIDS ENCODING THE SAME AND METHODS OF
ITILE OF INVENTION: USE
NUMBER OF SEQUENCES: 22
CORRESCONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       82 VGVLWFVSVTTGP------WGAVAISAGGESSLKCEDLKVGQYICKDPK-----IND 127
                                                                101 SAGGEESLKGEDLKVG----OYICKOPKINDATQEFVNCTNYTAHVSCFPAPNITCKDSS 156
                                                                                          223 TTGROASLKCEASAVPAPDFEWYRDJTRINSANGLEIKSTE---GOSSLTVTNVT-EEHY 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30 MRGPFKNLA-LLP--FSLPLLGGGGSGSEKVSVSKMAAAWPSGPSAPEA----VTAKL 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                       21; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5.6%; Score 80.5; DB 3; Length 456; 22.6%; Pred. No. 8.7;
                                                                                                                                                                     157 GNETHFIGNEVG-----FFKPISCRNVNGYSYKVAVALSLFLGWL 196
                       40; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
STREET: Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           <u>..</u> .. .. _ .. _
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/058,389A
FILING DATE: APTIL 9, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         39; Mismatches
  1 Similarity 29.9%; Pred. No. 5.3; 32; Conservative 14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 900
ATTORNEY/AGENT INFORMATION:
NAME: Jackson ESQ., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 1340-1-013N
TELECOMMUNICATION INFORMATION:
TELEFAX: 201-343-1684
                                                                                                                                                                                                                                                                                          Sequence 4, Application US/09058389A Patent No. 6130065
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 4: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 456 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 22.69
Matches 52; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein
DESCRIPTION: hENT1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hackensack
: New Jersey
RY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FRAGMENT TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 07601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM:
                                                                                                                                                                                                                                                                           US-09-058-389A-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-058-389A-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                       Matches
                                                                                                                                                                                                                                                     RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                  ô
                                                                                                                                                                                       g
                                                                                                         쉱
```

```
271 SNSQPTNESHSIKAILKNISVLAFSVCFIFTITIGMFPAVTVEVKSSIAGSSTW----E 325
                                                                          --- CINYTAHVSCFPAPNIICKDS-SGNETHFIGNEV 167
215 VIILTIICYLGLPRLEFYRYYQQJKLEGPGEQETKLDJISKGE----EPRAGKEESGVSV 270
                                                                                                                                                                                                                                168 GFFKPISC-RNVNGYSYKVAVALSLFLGWLGADRFYLGYPALGLLKFCTV 216
                                                                                                                                                                                                                                                                           :| |:|| | : : : : :| | | | : : | | | 372
                                                                      128 ATQEPVN---
```

Scarch completed: September 26, 2003, 17:29:34 Job time : 35 secs

```
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
```

OM protein - protein search, using sw model

Run on:

September 26, 2003, 17:23:47; Search time 27 Seconds (without alignments) 1507:467 Million cell updates/sec

US-09-852-100A-2 1439 Title: Perfect score:

1 MHILKGSPNVIPRAHGQKNT......TRLTRLSITNETFRKTQLYP 269 Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

566894 seqs, 151307093 residues Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Published_Applications_AA:

Database

/cgn2_6/ptodata/2/pubbaa/US07_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubbaa/US07_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubbaa/US06_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/PCTUB_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/US098_PUBCOMB.pep:*

/cgn2_6/ptodata/2/pubpaa/US104_NEW_PUH.ppp:*/cgn2_6/ptodata/2/pubpaa/US10A_PUHCOMB.pep:*/cgn2_6/ptodata/2/pubpaa/US10&_PUHCOMB.pep:*/cgn2_6/ptodata/2/pubpaa/US10&_PUHCOMB.pep:*/cgn2_6/ptodata/2/pubpaa/US10_NEW_PUH.pep:*/cgn2_6/ptodata/2/pubpaa/US10_NEW_PUH.pep:*/cgn2_6/ptodata/2/pubpaa/US10_NEW_PUH.pep:*/

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

/cgn2_5/pt.odata/2/pubbaa/US60_PUBCOMB.pep:*

SUMMARIES

Resuit No.	Score	% Query Match	% Query Match Length DB	DΒ	ID	Description
-	V & & I	100.0	597	תכ	US-09-852-100A-2	Sequence 2, April
7	1439	100.0	269	10	US-09-833-503A-2	Sequence 2, Appli
3	1439	100.0	269	15	US-10-199-881-2	
4	201	14.0	221	11	US-09-974-879-230	230
S	201	14.0	222	7	US-09-305-736-230	Sequence 236. App
9	200	13.9	221	10	US-09-833-503A-6	2
7	200	13.9	221	11	US-09-992-600A-82	82,
80	200	13.9	221	11	US-09-924-340-82	82
6	200	13.9	221	12	US-09-992-095B-82	82,
10	200	13.9	221	12	US-10-154-678-82	82,
11	200	13.9	221	12	US-08-999-570-82	82
12	200	13.9	221	15	US-10-000-489-82	82,
13	200	13.9	221	15	US-10-000-986-82	82,
14	200	13.9	221	15	US-10-199-881-6	Sequence 6, Appli
15	200	13.9	247	11	US-09-796-753-48	48

Sequence 50, Appl	Sequence 4, Appli	Sequence 4, Appli	Sequence 1018, Ap	Sequence 58, Appl	Sequence 631, App	Sequence 10938, A	Sequence 10935, A	Sequence 9371, Ap	Sequence 8693, Ap	Sequence 72, Appl	Sequence 61, Appl	Sequence 489, App	Sequence 13418, A	Sequence 27, Appl	Sequence 69, Appl	Sequence 58, Aprl	Sequence 58, Aprl	Sequence 10376, A	Sequence 2, Appli	Seguence 2, Appli	Sequence 17, Appl	Sequence 2, Appli	Sequence 28, Appl	Sequence 7, Appli	Sequence 8, Appli	Seguence 14515, A	Sequence 124, App	Sequence 92, Appl	Sequence 6200, Ap
0S-854-964-80 1	US-09-833-503A-4	US-10-199-881-4	US-09-925-301-1018	US-09-798-889-58	US-09-866-050A-631	. us-10-156-761-10938	. US-10-156-751-10936	US-10-156-761-9371	US-10-156-751-8693	US-09-808-502-72	US-09-800-198-61	US-09-925-297-489	US-10-156-751-13418	US-10-177-293-27	US-09-808-605-69	US-09-800-198-58	US-10-161-572-58	US-10-156-761-10376	US-10-054-044A-2	US-09-795-232-2	US-09-284-320-17	US-09-961-403-2	US-10-011-859-28	US-10-080-917-7	US-10-294-055-8	US-10-156-761-14515	US-10-191-813-124	US-09-800-198-92	US-09-738-626-6200
11	10	15	9	$\overline{}$:1	15	15	15	15	10	11	S	15	15	10	11	15	15	15	σ	Ξ	11	14	15	15	15	12	11	10
230	214	214	224	172	213	166	87	443	476	338	338	389	179	764	338	338	338	416	717	797	373	328	328	476	099	987	797	245	304
13.6	ي اح	9.5	ر. د	8.4	8.0	9.9	6.4	6.3	9.0	5.9	5.9	50 .0	رى 80	5.9	5.7	5.7	5.7	5.7	5.6	5.6	5.6	9.6	5.6	5.6	5.6	5.5	5.5	5.5	5.4
196	136.5	136.5	136.5	121	115.5	94.5	92.5	06	87	85	85	84.5	83.5	83	82.5	82.5	82.5	82	81	81	80.5	80	80	80	80	79.5	79	78.5	78
16	17	80 r:1	6.1	20	2:	22	23	54	25	26	27	28	29	30	31	32	33	3.4	35	36	37	38	39	0,	41	4.2	43	44	45

ALIGNMENTS

```
THILE OF INVENTION: Beca-amyloid Peptide-Binding Proteins and Polynucleotides Entitling of INVENTION: Beca-amyloid Peptide-Binding Proteins and Polynucleotides Entitling of INVENTION: Same
FILE WEFFRENCE: AHP981261p2
CURRENT APPLICATION NUMBER: US/09/852,100A
CURRENT FILING DATE: 2001-05-09
PRIOR FILING DATE: 1998-10-14
PRIOR APPLICATION NUMBER: US 60/104,104
PRIOR FILING DATE: 1998-10-13
PRIOR FILING DATE: 1998-10-13
PRIOR FILING DATE: 1999-10-13
PRIOR FILING DATE: 1999-04-15
PRIOR FILING DATE: 1999-04-16
PRIOR FILING DATE: 1999-04-16
PRIOR FILING DATE: 1999-04-16
PRIOR FILING DATE: 1999-04-16
                              Sequence 2, Application US/09852100A Patent No. US20020058267A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PatentIn version 3.0
US-09-852-100A-2
```

ΕĽ

Gaps . 0 Length 269; Indels DB 9; Query Match 100.0%; Score 1439; DB 9 Best Local Similarity 100.0%; Pred. No. 2e-135; Matches 269; Conservative 0; Mismatches 0 Query Match

ORGANISM: Homo sapiens

US-09-852-100A-2

.; O

1 MHILKGSPNVIPRAHGQKNTRRDGTGLYPMRGPFKNLALLPFSLPLLGGGGSGSGEKVSV 60

Š g ò

61 SKMAAAWPSGPSAPEAVTARLVGVLWFVSVTTGPWGAVATSAGGEESLKCEDLKVGQYIC 123

```
APPLICATION NUMBER: US 60/064,988 FILING DATE: 1997-11-07 APPLICATION NUMBER: US 60/064,987 FILING DATE: 1997-11-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 60/064,912
FILING DATE: 1997-11-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 60/064,983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 60/064,900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 230, Application US/09974879 Publication No. US20030028003A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                 100.0%;
                                                                                                                                                                                          SOFTWARE: PatentIn version 3.1 SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1997-11-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1997-11-07
                                                                                                                                                                                                                                                                                                                                                   Matches 269; Conservative
                                                                                                                                                                         NUMBER OF SEQ ID NOS: 45
                                                                                                                                                                                                                                                               ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                  Ouery Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
                                                                                                                                                                                                                              269
                                                                                                                                                                                                                                                                                 US-10-199-881-2
                                                                                                                                                                                                                                               TYPE: PRT
                                                                                                                                                                                                                                LENGIH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR
PRIOR
PRIOR
PRIOR
PRIOR
PRIOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR
PRIOR
PRIOR
PRIOR
                                                                                                                                                                                                                                                                                                                                                                                                                       g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6
                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Ozenberger, Bradley A
APPLICANT: Ozenberger, Bradley A
APPLICANT: Cashberger, Bradley A
APPLICANT: Lo, Ching-Hsiung F
APPLICANT: Lo, Ching-Hsiung F
APPLICANT: American Home Products Corporation:
TILLE OF INVENTION: No. US20020146760Alel G-Protein-Coupled Receptor::ike Proteins au
TILLE OF INVENTION: Same
FILE REFERENCE: AHP9315-000-00-000 PRIOR PAPLICATION NUMBER: US/95/833,503A
OURRENT FILING DATE: 2000-10-13
PRIOR APPLICATION NUMBER: 60/104,104
PRIOR FILING DATE: 1998-10-13
NUMBER OF SEO ID NOS: 6
SOFTWARE: Fatentin Vor. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2, Application US/10199881
Publication No. US20030096335A1
GENERAL INFORMATION:
APPLICANT: Wyeth
TITLE OF INVENTION: No. US20030096335A1cl G-Protein-Coupled Receptor-Like Proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SKMAAAWPSGPSAPFAVIARLVGVLWFVSVTTGPWGAVATSAGGEESLKCEDLKVGQY1C 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 KDPKINDAIQEPVNCTNYTAHVSCFPAPNITCKDSSGNETHFTGNEVGFFKPISCRNVNG 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YSYKVAVALSLFLGWLGADRFYLGYPALGLLKFCTVGFCGIGSLIDFILISMQ1VGPSDG 240
                                                                                                                                          181 YSYKVAVALSLFLGWLGADRFYLGYPALGLKRCTVGFCGIGSLIDFILLISWQIVGPSDG 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KDPKINDATQEPVNCTNYTAHVSCFPAPNITCKDSSGNETHFTGNEVGFFKPISCRNVNG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  181 YSYKVAVALSLFLGWLGADRFYLGYPALGLLKFCTVGFCGIGSLIDFILLISMQIVGPSDG 240
KDPKINDATQEPVNCTNYTAHVSCFPAPNITCKDSSGNETHFIGNEVGFFKPISCRNVNG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MHILKGSPNVIPRAHGQKNTRRDGTGLYPWRGPFKNLALLPFSLPLLGGGGSGSGGKVSV 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 269;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 1439; DB 1
100.0%; Pred. No. 2e-135;
iive 0; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          241 SSYIIDXYGTRLTRESITNETFRKTQLYP 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      241 SSYIIDYYGTRLIRLSITNETFRKTQLYP 269
                                                                                                                                                                                             SSYIIDYYGTRLTRISITNETFRKTQ1YP 269
                                                                                                                                                                                                            SYMIDYYCTRLTRESITNETFREGORP 269
                                                                                                                                                                                                                                                                                                                  Sequence 2, Application US/09833503A Patent No. US20020146760A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 100.
Matches 269; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                  US-09-833-503A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-833-503A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 3
US-10-199-881-2
                                                                                                                          181
                                                                                                                                                                                             241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61
                                                    121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO 2
                                                                                                                                                                                                                                                                                   RESULI 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   엄
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                    ò
                                                                                     g
                                                                                                                          ô
                                                                                                                                                       a
                                                                                                                                                                                             ò
                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
```

```
121 KDPKINDATQEPVNCTNYTAHVSCFPAPNITCKDSSGNETHFTGNEVGFFKPISCRXVNG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 SKMAAAWPSGPSAPEAVTARLVGVLWFVSVTTGPWGAVATSAGGEESLKCEDLKVGQYIC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 SKMAAAWPSGPSAPEAVTARLVGVLWFVSVTTGPWGAVATSAGGEESLKCEDLKVGQYIC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 KDPKINDATQEPVNCTNYTAHVSCFPAPNITCKDSSGNETHFTGNEVGFFKPISCRNVNG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MHILKGSPNVIPRAHGQKNITRRDGTGLYPMRGPFKNLALLPFSLPLJGGGGSGSGSKVSV 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181 YSYKVAVALSLFLGWLGADRFYLGYPALGLLKFCTVGFCGIGSLIDFILISMQIVGPSDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
FILE REFERENCE: AHP98165C1
CURRENT APPLICATION NUMBER: US/10/199, 881
CURRENT FILING DATE: US/20-18
PRIOR PFLICATION NUMBER: US/20-18
PRIOR FILING DATE: 1999-10-13
PRIOR FILING DATE: 1999-10-13
PRIOR FILING DATE: 1999-10-13
PRIOR FILING DATE: 2001-12-04
PRIOR FILING DATE: 2001-12-04
PRIOR FILING DATE: 2001-12-04
PRIOR FILING DATE: 2001-12-04
PRIOR FILING DATE: 1998-10-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 259;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PAPELICANT: ROSEN et al.
TITLE OF INVENTION: 125 Human Secreted Proteins
FILE REFRENCE: POZORDZ
CURRENT APPLICATION NUMBER: US/09/974.879
CURRENT FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: US 60/239,893
PRIOR APPLICATION NUMBER: US 09/818,683
PRIOR APPLICATION NUMBER: US 09/818,683
PRIOR FILING DATE: 2001-03-28
PRIOR FILING DATE: 1999-05-05
PRIOR FILING DATE: 1999-11-04
PRIOR APPLICATION NUMBER: US 60/064,911
PRIOR FILING DATE: 1999-11-04
PRIOR FILING DATE: 1999-11-04
PRIOR FILING DATE: 1997-11-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 1439; DB 1
Pred. No. 2e-135;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      241 SSYIIDYYGTRLTRLSIINETFRKTQLYP 269
```

÷

```
PAPLICANT: Ozenberger, Bradley A
APPLICANT: Ozenberger, Bradley A
APPLICANT: Carporation:
APPLICANT: Carporation
APPLICANT: Carporation
APPLICANT: Lo, Ching-Esung F
APPLICANT: Lo, Ching-Esung F
APPLICANT: Lo, Ching-Esung F
TILE OF INVENTION: No. US2020146760Alel G-Protein-Coupled Receptor-Like Protein:
TILE OF INVENTION: Same
TILE OF INVENTION: Same
TILE OF INVENTION: Same
TILE OF INVENTION: Same
CURRENT APPLICATION NUMBER: US/09/833,503A
PRIOR PLILING DATE: 1998-10-13
PRIOR FILING DATE: 1998-10-13
NUMBER OF SEQ ID NOS: 6
SECTION NOT: 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      135 CTNYTA - HVSC - - - FPAPNITCKDSSGNETHFTGNEVGFFKPISCRNVNGYSYKVAVA 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           135 CTNYTA--HVSC----FPAPNITCKDSSGNETHFTGNEVGFFKPISCRNVNGYSYKVAVA 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             112 CINSTSCMTVSCPRORYPA-NCTVRD----HVHCLGNRT-FPKMLYCNWTGGYKWSTALA 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      189 LSLFLGWLGADRFYLGYPALGLLKFCTVGFCGIGSLIDFILISMQIVGPSDGSSYI 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           189 LSLFLGWLGADRFYLGYPALGLLKFCTVGFCGIGSLIDFILLISMQIVGPSDGSSYI 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       39; Indels 12; Caps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     indels 12; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 222;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 221;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 14.0%; Score 201; DB 11; Bost Local Similarity 45.7%; Pred. No. 5.9e-12; Matches 53; Conservative 12; Mismatches 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Overy Match
Best Local Similarity 45.7%; Pred. No. 7.4e-12;
Matches 53; Conservative 12; Mismatches 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            . LOCATION: (222)
. OTHER INFORMATION: Xaa equals stop translation
US-09-336-736-230
                                 EARLIER FILING DATE: 1997-11-17
EARLIER APPLICATION NUMBER: 60/066,089
EARLIER APPLICATION NUMBER: 60.066,095
EARLIER FILING DATE: 1997-11-17
EARLIER FILING DATE: 1997-11-17
EARLIER FILING DATE: 1997-11-17
NUMBER OF SEQ ID NOS: 612
SEG: FARE PARENTIN NUMBER: 60/066,090
EARLIER FILING DATE: 1997-11-17
SEG ID NO 230
LENGTH: 222
           EARLIER APPLICATION NUMBER: 60/066,100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 6, Application US/09833503A Patent No. US20020146760A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CRGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: SITE
LOCATION: (184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 6
US-09-833-503A-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-833-503A-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 221
                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     dC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         : NAME/KEY: SITE
: LOCATION: (184)
: OIHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids US-09-974-879-230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               135 CTNYTA--HVSC----FPAPNITCKDSSGNETHFTGNEVGFFKPISCRNVNGYSYKVAVA 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       189 LSLFLGWLGADRFYLGYPALGLLKFCTVGFCGIGSLIDFILISMQIVGPSDGSSYI 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14.0%; Score 201; DB 11; Length 221; 45.7%; Pred. No. 5.9e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            39; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Feng et al.
TITLE OF INVENTION: 125 Human Societed Proteins
FILE REFERENCE: PROSOPI
CURRENT APPLICATION NUMBER: US/09/305,736
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRENT FILING DATE: 1999-05-05
EARLIER APPLICATION NUMBER: PCT/US99/23435
EARLIER FILING DATE: 1998-11-04
EARLIER FILING DATE: 1997-11-07
EARLIER APPLICATION NUMBER: 60/064,912
EARLIER FILING DATE: 1997-11-07
EARLIER FILING DATE: 1997-11-07
EARLIER APPLICATION NUMBER: 60/064,983
EARLIER FILING DATE: 1997-11-07
                  PRIOR FILING DATE: 1997-11-07
PRIOR APPLICATION NUMBER: US 60/064,984
PRIOR FILING DATE: 1997-11-07
PRIOR FILING DATE: 1997-11-07
PRIOR PELING DATE: 1997-11-07
PRIOR APPLICATION NUMBER: US 60/066,094
PRIOR APPLICATION NUMBER: US 60/066,090
PRIOR FILING DATE: 1997-11-17
PRIOR FILING DATE: 1997-11-17
PRIOR PELING DATE: 1997-11-17
PRIOR APPLICATION NUMBER: US 60/066,095
PRIOR FILING DATE: 1997-11-17
PRIOR PILING DATE: 1997-11-17
PRIOR PILING DATE: 1997-11-17
PRIOR FILING DATE: 1997-11-17
SECTION NUMBER: US 60/066,095
PRIOR FILING DATE: 1997-11-17
SECTION OF SECTION NUMBER: US 60/066,090
SECTION OF SECT
APPLICATION NUMBER: US 50/064,908
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         60/064,987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER: 60/064,908
1997-11-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EARLIER FILING DATE: 1997-11-07
EARLIER APPLICATION UNBER: 60/064,988
EARLIER FILING DATE: 1997-11-07
EARLIER APPLICATION NUMBER: 60/064,983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EARLIER FILING DATE:1997-11-07
EARLIER APPLICATION NUMBER: 60/064,908
EARLIER FILING DATE: 1997-11-07
EARLIER APPLICATION NUMBER: 60/064,984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EARLIER FILING DATE: 1997-11-07
EARLIER APPLICATION NUMBER: 60/064,986
EARLIER FILLIG DATE: 1997-11-07
EARLIER APPLICATION NUMBER: 60/066,094
EARLIER FILING DATE: 1997-11-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 230, Application US/09305736 Publication No. US2003008807841
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 45.7
Matches 53; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-305-736-230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
```

```
53; Conservative
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 53; Conserva
                               ; FEATURE:
: NAME/KEY: SIGNAL
; :OCATION: 1.32
US-69-524-340-82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: SIGNAL LOCATION: 1..32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-992-095B-82
                                                                                                                                                                     Query Match
Best Local Si
Matches 53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ô
                                                                                                                                                                                                                                                                                         à
                                                                                                                                                                                                                                                                                                                                          3
                                                                                                                                                                                                                                                                                                                                                                                                 Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    135 CTNYTA--HVSC----FPAPNITCKDSSGNEIHFIGNEVGFFKPISCRNVNGYSYKVAVA 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               189 LSLFLGWLGADRFYLGYPALGLIKFCTVGFCGIGSLIDFTLISMQIVGPSDGSSYI 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                              US-099-0600A-82
US-09-992-600A-82
US-09-992-600A-82
Sequence 82, Application US/09992600A
Publication No. US20030027161A1
GENERAL INFORMATION:
APPLICANT: Benjanka: Hiroaki
TITLE OF INVENTION: Stephane
TILE REFERENCE: 91.US4.DIV
CURRENT APPLICATION NUMBER: US/09/992,600A
FRIDE REFERENCE: 91.US4.DIV
CURRENT APPLICATION NUMBER: US/09/992,600A
PRIOR FILING DATE: 2001-01-03
PRIOR FILING DATE: 2001-03-06
PRIOR FILING DATE: 2001-08-06
PRIOR FILING DATE: 2001-06-29
PRIOR FILING DATE: 2001-06-25
PRIOR FILING DATE: 2001-06-25
PRIOR FILING DATE: 2001-06-25
PRIOR FILING DATE: 2001-06-25
PRIOR PRIOR DATE: 2001-06-25
PRIOR DATE: 2001-06-25
PRIOR PRIOR DATE: 2001-06-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 82. Application US/09924340

Publication No. US2003002724841

GENERAL INFORMATION.

APPLICANT: Bejanin, Stephane
APPLICANT: Tanaka, Hiroaki
TILE OF INVENION: HUMAN CONAS AND PROIEINS AND USES THEREOF
FILE REFERENCE: 91.US2.REG
CURRENT FILING DATE: 2001-08-06

CURRENT FILING DATE: 2001-08-06

PRIOR PLICATION NUMBER: US 60/305,456

PRIOR FILING DATE: 2001-06-29

PRIOR PLICATION NUMBER: US 60/302,277

PRIOR PLICATION NUMBER: US 60/298,698

PRIOR PLICATION NUMBER: US 60/293,574

PRIOR FILING DATE: 2001-06-15

PRIOR FILING DATE: 2001-06-15

PRIOR FILING DATE: 2001-06-15

SOFTWARE: JPatent
SEQ ID NO 82

LENGHH: 221

TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   39; Indels 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 221;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 45.7%; Pred. No. 7.4e-12;
Matches 53; Conservative 12; Mismatches 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRI
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: SIGNAL LOCATION: 1..32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-992-600A-82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-924-340-82
```

СЪ

```
135 CTNYTA--HVSC----FPAPNITCKDSSGNEIHFTGNEVGFFKPISCRNVNGYSYKVAVA 188
                                                                                                                                                                135 CINYTA--HVSC----FPAPNITCKDSSGNETHFTGNEVGFFKPISCRNVNGYSYKVAVA 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               112 CINSTSCMTVSCPRQRYPA-NCTVRD----HVHCLGNRT-FPKMLYCNWTGGYKWSTALA 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           189 LSLFLGWLGADRFYLGYPALGLLKFCTVGFCGIGSLIDFILISMQIVGPSDGSSYI 244
                                                                                                                                                                                                                                     189 LSLFLGWLGADRFYLGYPALGLLKFCTVGFCGIGSLIDFILISMQIVGPSDGSSYI 244
                                                                                                                                                                                                                                                                          APPLICANT: Tenaka, Hiroki,
APPLICANT: Tenaka, Hiroki,
TIILE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREDF
FILLE REPERENCE: 91 US5.DIV
CURRENT APPLICATION NUMBER: US/09/92,095B
CURRENT FILING DATE: 2003-02-20
PRIOR PFLICATION NUMBER: US 09/924,340
PRIOR FILING DATE: 2001-08-06
PRIOR PRIOR DATE: 2001-08-06
PRIOR APPLICATION NUMBER: PCT/IB01/0175
PRIOR APPLICATION NUMBER: US 60/305,456
PRIOR PILING DATE: 2001-07-03
PRIOR FILING DATE: 2001-07-03
PRIOR FILING DATE: 2001-06-29
PRIOR FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: US 60/298,698
PRIOR FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: US 60/293,574
PRIOR APPLICATION NUMBER: US 60/293,574
SPRIOR FILING DATE: 2001-06-15
NUMBER OF SEQ ID NOS: 112
SEQ ID NO 82
LENGHI = 221
LENGHI = 221
ch 13.9%; Score 200; DB 11; Length 221;
1 Similarity 45.7%; Pred. No. 7.4e-12;
53; Conservative 12: Mismatches 39; Indeis 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 221;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13.9%; Score 200; DB 12; Length 22 45.7%; Pred. No. 7.4e-12; tive 12; Mismatches 39; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-992-095B-82
Sequence 82. Application US/0992095B
Publication No. US20030157485A1
GENERAL INFORMATION: Stephane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 10
18.10.154-678-82
Sequence 82, Application US/10154678
Publication No. US20030162186A1
GENERAL INFORMATION: Stephane
APPLICANT: Benjanin, Stephane
APPLICANT: Tanaka, Hiroaki
```

Ŋ

5

Gaps

12;

Indels

```
135 CTNYTA--HVSC----FPAPNITCKDSSGNETHFIGNEVGFFKPISCRNVNGYSYKVAVA 198
                                                                                                                                                      112 CINSTSCMIVSCPRORYPA-NCIVRD----HVHCLGNRT-FPKMLYCNWIGGYKWSTALA 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                135 CINYTA--HVSC----FPAPNITCKDSSGNETHFIGNEVGFFKP;SCRNVNGYSYKVAVA 186
                                                                                                                                                                                                               189 LSLFLGWLGADRFYLGYPALGLLKFCTVGFCGIGSLIDFILISMQIVGPSDGSSYI 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Benjanin, Stephane
APPLICANT: Benjanin, Stephane
APPLICANT: Tanaka, Hiroaki
TTLEOF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF
FILE MEFFRENCE: 91.065.DIV
CURRENT APPLICATION NUMBER: US/10/000,489
CURRENT APPLICATION NUMBER: US/00/11.14
PRIOR FILING DATE: 2001-08-06
PRIOR FILING DATE: 2001-08-06
PRIOR FILING DATE: 2001-08-06
PRIOR FILING DATE: 2001-08-06
PRIOR APPLICATION NUMBER: US 60/305,456
PRIOR FILING DATE: 2001-08-06
PRIOR PRIOR APPLICATION NUMBER: US 60/302,277
PRIOR PELING DATE: 2001-06-29
PRIOR FILING DATE: 2001-06-29
PRIOR FILING DATE: 2001-06-15
PRIOR SPELICATION NUMBER: US 60/293,574
PRIOR APPLICATION NUMBER: US 60/293,574
PRIOR APPLICATION NUMBER: US 60/293,574
PRIOR SPELICATION NUMBER: US 60/293,574
PRIOR SPELICATION NUMBER: US 60/293,574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Benjanin, Stephane
APPLICANT: Tanaka, Hiroaki
TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF
FILE REFERENCE: 91.0459.DIV
CURRENT APPLICATION NUMBER: US/10/000,986
CURRENT FILING DATE: 2001-11-14
PRIOR FILING DATE: 2001-08-06
PRIOR FILING DATE: 2001-08-06
PRIOR FILING DATE: 2001-08-06
         sest Local Similarity 45.78; Fred. No. 7.4e-12;
Matches 53; Conservative 12; Mismatches 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match
Best Local Similarity 45.7%; Pred. No. 7.4e-12:
Matches 53; Conservative 12; Mismatches 39;
                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 82, Application US/10000489 Publication No. US20030092011A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-10-000-985-82

Sequence 82. Application US/10000986

Publication No. US/20030096247A1

GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; NAME/KEY: SIGNAL
; LOCATION: 1..32
US:10-000-489-82
                                                                                                                                                                                                                                                                                                                                                                                             US-10-000-489-82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 82
LENGTH: 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 13
                                                                                                   ó
                                                                                                                                                         å
                                                                                                                                                                                                                  ζ
                                                                                                                                                                                                                                                               B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           112 CINSISCMIVSCPRQRYPA-NCIVED----HVHCLGNRT-FPRMLYCNWIGGYKWSIALA 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              135 CINYTA--HVSC----FPAPNIICKDSSGNETHFTGNEVGFFKPISCRNVNGYSYKVAVA 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          189 LSLFLGWLGADRFYLGYPALGLLKFCTVGFCGIGSLIDFILISMQIVGPSDGSSYI 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Benjanin, Stephane
APPLICANT: Benjanin, Stephane
TILEO E INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREDE
FILE REFERENCE: G-09JUSOBOJU
CURRENT APPLICATION NUMBER: US/09/999,570
CURRENT APPLICATION NUMBER: US/09/999,570
PRIOR PILING DATE: 2001-06-14
PRIOR PELING DATE: 2001-08-06
PRIOR FILING DATE: 2001-08-06
PRIOR FILING DATE: 2001-08-06
PRIOR PLING DATE: 2001-08-06
PRIOR PLING DATE: 2001-08-06
PRIOR PLING DATE: 2001-08-06
PRIOR APPLICATION NUMBER: US 60/305,456
PRIOR PLING DATE: 2001-06-09
PRIOR PLING DATE: 2001-06-15
PRIOR PLING DATE: 2001-06-15
PRIOR PLING DATE: 2001-06-15
PRIOR FILING DATE: 2001-06-15
PRIOR FILING DATE: 2001-06-15
PRIOR PLING DATE: 2001-06-15
PRIOR PLING DATE: 2001-06-15
PRIOR PLING DATE: 2001-06-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 221;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 12; Length 221;
TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match
13.9%: Score 200; DB 12; Best Local Similarity 45.7%; Pred. No. 7.4e-12;
Matches 53; Conservative 12; Mismatches 39;
                  FILE REFERENCE: 182.051.REG
CURRENT APPLICATION NUMBER: US/15/578
CURRENT FILING DATE: 2002-10-15
PRIOR PELICATION NUMBER: US/924,340
PRIOR FILING DATE: 2001-08-06
PRIOR FILING DATE: 2001-08-06
PRIOR FILING DATE: 2001-08-06
PRIOR FILING DATE: 2001-08-29
PRIOR FILING DATE: 2001-06-29
PRIOR FILING DATE: 2001-06-15
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 112
SOFTMARE: JPALENT
SEG ID NOS: 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13.9%; Score 200;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 82, Application US/0999570 Publication No. US20030170628A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 112
SOFTWARE: JPatent
SEQ ID NO 82
LENGTH: 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; NAME/KEY: SIGNAL
; LOCATION: -32..-1
US-10-154-678-82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-999-570-82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-999-570-82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
```

a ò

ò q 'n

Gaps

Indels 12;

9

```
135 CTNYTA--HVSC----FPAPNITCKDSSGNEIHFTGNEVGFFKPISCRNVNGYSYKVAVA 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 13.9%; Score 200; DB 11; Length 247; Best Local Similarity 45.7%; Pred. No. 8.6e-12; Matches 53; Conservative 12; Mismatches 39; Indels 1:
                                                                                                              PRICE REPERENCE: 783.227-999
CURRENT PAPLICATION: SECRETED PROTEINS AND USES THEREOF
FILLE REFERENCE: 783.227-999
CURRENT PAPELICATION NUMBER: US/09,796,753
CURRENT FILING DATE: 1001-03-01
PRIOR APPLICATION NUMBER: 09/223,094
PRIOR PELICATION NUMBER: 09/223,696
PRIOR FILING DATE: 1998-10-30
PRIOR FILING DATE: 1998-12-30
PRIOR FILING DATE: 1998-12-30
PRIOR FILING DATE: 1998-12-30
PRIOR FILING DATE: 1999-12-36
PRIOR FILING DATE: 1999-02-26
PRIOR FILING DATE: 1999-03-04
PRIOR FILING DATE: 1999-05-14
PRIOR FILING DATE: 1999-06-18
PRIOR FILING DATE: 1999-06-18
PRIOR FILING DATE: 1999-06-18
PRIOR FILING DATE: 1999-06-19
PRIOR FILING DATE: 1999-06-30
PRIOR FILING DATE: 1999-07-30
PRIOR APPLICATION NUMBER: 09/414,071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: 09/516,745
PRIOR FILING DATE: 2000 03-01
PRIOR FILING DATE: 2000 03-01
PRIOR FILING DATE: 2000 03-01
PRIOR FILING DATE: 2000 05-14
PRIOR FILING DATE: 2000 06-19
PRIOR APPLICATION NUMBER: 09/59,596
PRIOR FILING DATE: 2000 06-22
PRIOR FILING DATE: 2000 07-31
PRIOR FILING DATE: 2000 07-31
PRIOR FILING DATE: 2000 07-31
PRIOR PAPLICATION NUMBER: 09/606,565
PRIOR PAPLICATION NUMBER: 09/606,565
PRIOR PAPLICATION NUMBER: 09/606,565
PRIOR PAPLICATION NUMBER: 09/606,565
PRIOR PAPLICATION NUMBER: 09/606,517
PRIOR PAPLICATION NUMBER: 09/606,317
PRIOR FILING DATE: 2000 06-29
PRIOR FILING DATE: 2000 06-29
PRIOR PAPLICATION NUMBER: 09/606,317
PRIOR PAPLICATION NUMBER: 09/606,317
PRIOR FILING DATE: 2000 06-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MBER: 09/665,666
2000-09-20
MBER: 09/677,751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2000-08-30
                                              oublication No. US20030027998A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR FILING DATE: 2000-09 PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR FILING DATE: 2000-0° NUMBER OF SEQ ID NOS: 162 SEQ ID NO 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; ORGANISM: Homo sapiens
US-09-796-753-48
                                                                            GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 6, Application US/10199881

Fublication No. US20030096356A1

GENERAL INFORMATION:

APPLICATION No. US20030096356A1cl G-Frotein-Coupled Receptor-Like Proteins and TITLE OF INVENTION:

TITLE INVENTION:

TITLE OF 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             135 CTNYTA--HVSC----FPAPNITCKDSSGNETHFTGNEVGFFKPISCRNVKGYSYKVAVA 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                135 CINYTA--HVSC----FPAPNITCKDSSGNETHFTGNEVGFFKPISCRNVNGYSYKVAVA 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   112 CINSTSCMTVSCPRORYPA-NCTVRD----HVHCLGNRT-FPKMLYCNWTGGYKWSTALA 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    189 LSLFLGWLGADRFYLGYPALGLLKFCTVGFCGIGSLIDFILJSMQIVGPSDGSSYI 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              189 LSLFLGWLGADRFYLGYPALGLLKFCTVGFCGIGSLIDFILJSMQIVGPSDGSSYl 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ouery Match 13.9%; Score 200; DB 15; Length 221; Best Local Similarity 45.7%; Pred. No. 7.4e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 221;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 39; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          39; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13.9%; Score 200; DB 15; 45.7%; Pred. No. 7.4e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
13.9%; Score 200; DB
Best Local Similarity 45.7%; Pred. No. 7.4e
Matches 53; Conservative 12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12; Mismatches
                                 PRIOR APPLICATION NUMBER: US 60/305,456
PRIOR FILING DATE: 2001-07-13
PRIOR APPLICATION NUMBER: US 60/302,277
PRIOR PILING DATE: 2001-06-29
PRIOR FILING DATE: 2001-06-15
PRIOR PRICATION NUMBER: US 60/294,698
PRIOR PILING DATE: 2001-06-15
PRIOR PLILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 112
SOFTWARE: UPatent
SEQ ID NO 82
LENGTH: 221
PRIOR FILING DATE: 2001-08-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 53; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRI
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-10-000-986-82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 15
US-09-796-753-48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 14
US-10-199-881-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; ORGANISM: HC
US-10-199-881-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
```

ò

ò

	•
VSOPRORYPA-NO:	A THE PROPERTY OF THE PROPERTY
TECHT	
Z	
38	

244	
189 LSLFLGWLGADRFYTGYPALGLLKFCTVGFCGIGSLIDF11.1SMQ1VGPSDGSSYI	
IDFILISMO	
TVGFCGIGSL	-
ALGLIKFCT'	-
GADRFYLGYP	
189 LSLFLGWL	-
18	

Çy D

a

¹⁹² LSITLGGFGADRFYLGQWREGLGKLFSFGGLGIWTLIDVLLIGVGYVGPADGSLYI 247

Search completed: September 26, 2003, 17:28:52 Job time : 28 secs

```
GenCare version 5.1.6
Copyright (c) 1993 - 2003 Compuges Ltd.
```

OM protein - protein search, using sw model

September 26, 2003, 17:22::1 : Search time 49 Seconds (without alignments) 691:613 Million cell updates/sec Run on:

....TRLTRLSITNETFRKTOLYF 269 US-09-852-100A-2 1439 1 MHILKGSPNVIPRAHGOKNT.. Title: Perfect score: Sequence:

BLCSCM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283308 seqs, 96168682 residues Searched:

263308 Total number of hits satisfying chosen parameters:

Minimum DB scg length: 0 Maximum DB scg length: 2000000003

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_76:* Database

1: pirl: * 2: pir2: * 3: pir3: * 4: pir4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMARTE

		ans			SUMMARIES	
Result No.	Score	Query	Length	DB	C1	Description
1	67		573	. ~	S446C5	CO2F5.3 protein -
N	159.5		753	(7)	128797	hypothetical prote
m	95	9	369	~	H75286	
4	92	œ œ	456	7	555661	hypothetical profe
5	91	9.	1324	, - 1	VGIH59	E2 glycoprotein pr
9	89.5	Θ.	069	7	T08634	hypothetical prote
7	87.5		547	7	H75632	Na(+)-linked D-ala
80	87.5	9	1207	~	T23754	hypothetical prote
6	85.5	δ.	348	-	S20911	dehyd
10	84	Ŋ.	446	7	T35005	probable integral
11	83.5	5.8	487	7	C70574	
12	83	5.8	137	7	B75447	cal p
13	83	5.8		-	S32521	alcohol dehydrogen
14	83	5.8		7	ввис	complement factor
15	83	5.8	_	7	T10729	transferrin-like p
16	82.5	5.7		7	304776	limbic system asso
17	9.2	5.7	60 *	C)	T03788	Laccase (EC 1.10.3
18	81.5	5.7		7	737164	probable meneckyde
19	81.5	5.7	_	7	AG2695	conserved hypothet.
20	81.5	5.7	_	7	G97477	hypothetical prote
21	81	9.9		7	G90388	thermopsine precur
22	81	5.6		7	A81850	probable integral
23	81	5.6		~1	C81092	oxalate/formate an
24	81	5.6		7	36	beta-D-glucosidase
25	81	5.6	_	7	8	hypothetical prote
56	0	5.6		~	D83595	netical
27	80.5	9.6	223	7	F72803	
28	0	5.6	-	7	5408	in-tyros:
59	80	5.6		~	T01466	iron-sulfur cofact

6 õ 3 $\overset{>}{\circ}$ ã WESHIT 2
TABLE
TAB

Section of the sectio		12.4 5.4 5.4
erc oute ine ine ine inc inc inc inc inc	C2-Feb-2001	Gaps K GKCLK
chitosanase (insulin-like tracylalycer probable inte auxilin - box genome polypt polyp	^	%; Score 167.5; DB 2: i.ength 573; 23; Mismatches 57; Indels 49; Gaps 23; Mismatches 57; Indels 49; Gaps ESEKCEDIKVGQYICKDP
chi ins tri pro pro gen gen dyn hyp hyp hyp hyp hyp hyp hyp hyp hyp hyp	change 	Length Indels
	5 #text. C02F5. cmology op op op op	57; 57; 57; 57; 57; 57; 57; 57; 57; 57;
	S 20-Feb-1995 1993 ns cosmid C(89607; PID:9 6017; PID:9 factor Tu hor factor Tu hor factor Tu hor factor Tu hor factor Tu hor	1.3e- ches ICKDP- : :
252 4831 4132 4133 4133 4133 4133 4133 4133 41	iegans sion 20-Feb sion 20-Feb way 1993 elegans cos elegans cos 10:9289607; 0/3; 503/2 ton factor ation factor ation factor motif A (P	imilarity 27.9%; Pred. No. 1.3e; Conservative 23; Mismatches VTGPWGAVATSAGGEESLKCEDLKVGQYICKDP I I I I I I I I I I I I I I I I I I I
JC7852 A41927 LIP67 B10514 S68983 GNWVJE GNWVJE GNWVJE GNWVJE GNWVJE GNWVJE GNWVJE GNWVJE GNWVJE GNWVJE GNWVJE GNWVJE GNWVJE GNWVJE FN 28218 FN 3681 FN 3681 F	ALIG enorhabditis elegans ditis elegans fitis elegans *Sequence_revision 2 L Data Library, May nce of the C. elegan \$44603 // ND> EMBL:L14745; NID:928 1471; 363/3; 390/3; 5 lation elongation fa ing; nucleotide bind nslation elongation ectide-binding motif 'P-binding NXXD motif	SCO 23; SLKCED ::
a	ditis e legans ce_revi ce_revi Library the C. 4745; N 4745; N 6100gat cleotid cleotid nelong nelong ng NXXD	11.6%; 27.9%; ive AGGEES
28	Caenorhabditis abditis elegans 5 *Sequence_re 5 MBL Data Libra uence of the C : \$44603 ary NA AND : EMBL:L14745; saltion elong nding; nucleot ranslation elong cleotide-bindi GTP-binding NX	imilarity 27. Conservative VTTGPWGAVATSAGG : VTTGPWGAVATSAGG
សសលស្តសសសសសសសសសស ភស្តសស្តសស្តសស្តស្តស្តស	Caen rhabdi 995 #Si 605 #Si 605 #Si 605 #Si equency equency equency equency equency equency equency equency equency and and and and and and and and and and	h Similarity 50: Conser C VTTGPWGAV : i
7474 7479 7474 7479 7474 7479 7479 7479 7479 7479 7479 7479 7479 7479	procein - Sa Caenor - Caeno	7 S S S S S S S S S S S S S S S S S S S
и и и и и и и и и и и и и и и и и и и	PESULT 1 \$34505 (C.22P.3 protein - Caenorhabditis elegans C.Species: Caenorhabditis elegans A.Bescription: Sequence of the C. elegans cosmid CO2F5. A.Bescription: Sequence of the C. elegans cosmid CO2F5. A.Bescription: Sq4605 A.Bescription: Sq4603 A.Bescription: Sq4605 A.Bescription: Sq4605 A.Bescription: Sq405 A.Bescription: Caenorhabditis A.Bescriptio	Query Best 1 Matcho
	সজেণ্ডণ্ডল জ ৰৰৰৰৰৰক্তৰ্ তত দুদ্দ	3 8

qq

염

δ

QQ

ò

```
E2 glycoprotein precursor - murine hepatitis virus (strain A59)
N'Alternate names: peplomer glycoprotein; spike glycoprotein
C:Species: murine hepatitis virus, MHV
C:Decies: murine hepatitis virus, MHV
C:Date: 31.Mar.1989 #sequence_revision 31.Mar.1989 #text_change 12-Apr-1996
C:Accession: A7740
C:Date: 31.Mar.1989 #sequence_revision 31.Mar.1989 #text_change 12-Apr-1996
C:Accession: A77402
M:Luyines Williams Willi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A.Residues: 1.456 <TEL>
A.Cross-references: GB:UZ0824; NID:g695172; PIDN:AAC13854.1; PID:g695239
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, February 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A. Moleculo Lype: genomic RNA
A. Residues: 1-124 < LUY>
C. Superfamily: coronavirus E2 glycoprotein
C. Keywords: glycoprotein: transmembrane protein
F.1-16/Jonain: signal sequence #status predicted <SIG>
F.17-713/4/Product: 90B glycoprotein #status predicted <EGS>
F.718-1324/Product: 90B glycoprotein #status predicted <EGS>
F.718-1324/Product: 90A glycoprotein #status predicted <FNN>
F.716-1286/Domain: transmembrane #status predicted <TNN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              66 TGYYPVDGSKFRNLALTGTNSVSLSWFQPPYLNQFNDGIFAK--VQNLKTSTPSGATAYF 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                47 LGGGGSGSGEKVSVSKMAAAWPSGPSAPEAVTARLVGVLWFVSVTTGPWGAVATSAGGEE 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          107 S----LKCEDLKVGQYIC-KDPKINDATQEPVNCTNYTAHV-----SCFPAPNTTCKDS 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            74 PEAVTARLVGVLWFVSVTTGPWGAVATSAGGEESLKCEDLKVGQY-ICKDPKINDATQEP 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C.Species: equine herpesvirus 2
C.Species: equine farpesvirus 2
C.Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 08-Oct-1999
C.Accession: 55561
F.Tello: The DNA sequence of equine herpesvirus 2.
A.Tille: The DNA sequence of equine herpesvirus 2.
A.Reference number: 555594; MUID:95302501; PMID:7783207
A.Reference number: 555594; MUID:95302501; PMID:7783207
A.Reference number: 555594; Muid:95302501; PMID:7783207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30 DGLMRALCEGLRVGEEDCARFVLYGVAYWQGGRCPEWVAHITRCADLSCFAIY..LTCHRS 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25 TGLYPMRG-PFKNLALLP------FSLPLLGGGGSGSGEKVSVSKMAAAWPSGPSA-- 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Katch 6.3%; Score 91; DB 1; Length 1324; Local Similarity 23.6%; Pred. No. 13; es 59; Conservative 27; Mismatches 94; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6.4%; Score 92; DB 2; Length 456; 26.2%; Pred. No. 3.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    156 SGNETHFIGNEVGFFKPISCRNVNGYSYKVAVALSLFLGW 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11: Mismatches
                                                                                                                                                                                                                                                                                                                      hypothetical protein 66 - equine herpesvirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 26.29
Matches 42; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3
                                                   a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ΩΩ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            े
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: GB:AE002064; GB:AE000513; NID:96460114; PIDN:AAP118B0.1; PID:3646014
A;Experimental source: strain R1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hypothetical protein - Deinococcus radiodyrans (strain R1)
(Species: Danococcus radiodurans
(Species: Danococcus radiodurans
(Spaces)
(Spa
                                                                                                                                                                                                                                                                                                                      A.Map position: 1
A.Introns: 53/2; 81/3; 117/1; 250/3; 274/2; 357/3; 443/2: 485/3; 544/3; 585/3; 637/2
                                  A;Residues: 1-753 <GAT>
A;Cross-references: EMBL:AF0C3740; PIDN:AAC48141.1; GSPDB:GN00C19; CESF:C41D11.5
A;Experimental source: strain Bristol N2; clone C41D11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ------VSVITGPWGAVATSAGGEESLKCEDLKVGQYICKDPKINDATQEPVNCTNY 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               157 -----PQESRTTVYSAAPQTDAWGDPVRPAPPAPVKPVRGQMGQSNGPAGLPVREDIA 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 104 GEESLKCE---DLKVGQYJCKDPKINDATQE----PVNCINYTA------HVSCF 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   284 GSAGLICIFPGDCRIGDIV----KVNCISRKGCPNPVSRNNVEAVCRFCWQLLPGDYDCE 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                146 PAPNITCKDS-----SGNETHFTGNEVGFFKPISCRNVNGYSYKVAVALSLFLGWIGA 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               64 PSGNAPSWVDEVLSSSSSAPRPVEGRHGQTADPAQNPAGTAPGSGWDHWPQTDAAKDLRL 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       139 TAHVSCFPAPNITCKDSSGNETHFTGNEVGFFKPISCRNVNGYSYK------- 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----VAVALSLFLGWLGADRFYLGYPALGLLKF-CTVGF------CGIGSLI--- 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16 GQKNTRRDGTGLYPM----RGPFKNLALLPFS-LPLLGGGSGSGSKK---VSVSKMAAAW 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11 GRLARQRKGLDFRPVAEGERGPV-----FSPTPPFGGRNSSPVRRVLSVMTDKDKDRDAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   124 PGDPPRPAPPSFDSDDWAARAT--GGE------VRDPGGRD-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 21.7%; Pred. No. 1.1;
Matches 73; Conservative 27; Mismatches 95; Indels 142; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 2; Length 753;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          199 DRFYLGYPALGLIKFCTVGFCGIGSLIDFILISMQIVGPSDGS 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 226 --DFILISMQIVGPSDGSSYII------DY-YGTR 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11.1%; Score 159.5; DB 2
28.2%; Pred. No. 8.6e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
tes 46; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Residues: 1-309 <WHI>A; Cross-references: GB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Status: preliminary
A;Molecule type: DNA
                                                                                                                                                                                                                                                             A; Gene: CESP:C41D11.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Accession: H75286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Gene: DR2326
A:Map position: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C; Genetics:
                                                                                                                                                                                                                     C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Loca
Matches
```

qq

2 g ò

ò

ga

qq

ò g

9

```
Connor, R.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Helroyd, Eajandeam, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
A.Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Harrell, B.G.
A.Richere number: A70500; MUID:98295987; PMID:9634230
A.Accession: C70574
A.Scession: C70574
A.Status: preliminary; nucleic acid sequence not shown; translation not shown
A.Residues: 1-487 <COL>
A.Residues: 1-487 <COL>
A.Experimental source: strain H37Rv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          159 ETHFTGNEVGFFKPISCRNVNGYSYKVAVALSLFLGWLGADRFYLGYPALGLLKFCTVGF 218
                                                               106 LIVLGYGFVGGIGLGIGYISPVSTLIKWFPDRPG-----MATGIAIMGFGGGALIASPWS 160
                                                                                                                                                                                                                                             127 DATQEP-----VNCTNYIAHVSCF--PAPNITCKDSSGNETHFTGNEVGFFKPISCRN 177
                                                                                                                                                                                                                                                                                                                                                           178 VNGYSYKVAVALSLFLGW-----LGADRFYLGYPALGILKFCTVGFCGIGSLIDFILIS 231
                                                                                                                                                                                                                                                                                                                                                                                                                    281 MAGR------FGWSSASDLIGRKNIYRVYLGVGALMYTLIALFGDSSKPLFVLCA 329
         39 LLPFSLPLiggggsgsgsgkysvskmaaawpsgpsapeaviaklygvlwf--vsvttgpwg 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              B DERLIREDIGYHKGLHSRQLQMIALGGAIGTGLFLG--AGGRLASAGPG----FLVYGI 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    probable aroF2 protein - Mycobacterium tuberculosis (strain H37RV)
C:Species: Mycobacterium tuberculosis
C:Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   40; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          219 CGIGSLIDFILISMQIVG-----PSDGS--SYIIDYYGTRL 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CGI----FVFLILRALGELVLHRPSSGSFVSYAREFYGEKV 98
                                                                                                                            AVATSAGGEES------LKCEDLKVGQYICKDPK----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 5.8%; Score 83.5; 1 Bost Local Similarity 26.5%; Prod. No. 19; Matches 27; Conservative 16; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              232 MQIV----GPSDGSSYIIDYYGT 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      330 LVVVSFYGGGFATAPAYLKDLFGT 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Argene: aroP2
C;Superfamily: arginine permease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C: Accession: C70574
                                                                                                                                                                                   161
                                                                                                                                                                       gg
                                                                                                                                                                                                                                                                                                 Ω
                                                                                                                                                                                                                                                                                                                                                                 Š
                                                                                                                                                                                                                                                                                                                                                                                                                    Ď,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ñ
                                                                                                                         ò
                                                                                                                                                                                                                                       ò
                           C:Species: Kluyveromyces marxianus var. lactis, Candida sphaerica
C:Date: 20-Apr-2006 #sequence_revision 20-Apr-2006 *text_change 20-Apr-2000
C;Accession: S2011; S19804
R:Shain, D.H.: Salvadore, C.:. Denis, C.:.
Mol. Gen. Genet. 232, 479-488, 1992
A:Title: Evolution of the alcohol dehydrogenase (ADH) genes in yeast: characterization data. Reference number: S20911; MUID:92269769; PMID:1588917
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 probable integral membrane transporter - Streptomyces coelicolor
C.Species: Streptomyces coelicolor
C.Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 17-Mar-2000
C.Accession: T35005
R.Seeger, K.J.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
B.M.Reference number: 221564
A.Reference number: 221564
alcohol dehydrogenase (EC 1.1.1.1) II - yeast (Kluyveromyces marxianus var. lucuis)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Residues: 1.446 <SEE>
A; Cross-references: EMBL:AL034443; PIDN:CAA22367.1; GSPDB:GN00070; SCOEDB:SC4B5.13
                                                                                                                                                                                                                                                                                                                                                                                                              C;Superfamily: alcohol dehydrogenase; long-chain alcohol dehydrogenase homology C;Reywords: alcohol metabolism; metalloprotein; NAD; oxidoreductase; zinc F;29-336/Domanin: long-chain alcohol dehydrogenase homology zLADH> F:173-202/Region: beta-alpha-beta NAD binding foid F:173-202/Region: beta-alpha-beta NAD; C(Cys, His, Cys) #status predicted F:98,101,104,112/Binding site: zinc, noncatalytic (Cys, His, Cys) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ν.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ARLVGV-----LWFVSVTTGPWGAVATSAGGEESLKCEDLKV-------------------1:5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----GOYICKDPKINDATGEPVNCTNYTAH-----VSCFPAPNITCKDSSGNETRFIGN 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EVGFFKPISCRNVNGYSYKVAVALSLFLGWLG--AD-RFYLGYPALGLLKFCTVGFCGTG 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              266 VVLVGLPRDAKCKSDVFTQVVKSVSIVGSYVGNRADTREALDFFRAGLV-HAPIKIVGLS 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   92 KWLNGSCMSCEYCELSNESNCPDADLSGYTHDGSFQQYATADAVQAARIPKGTDLAEVAP 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19 NTRRDG---TGLYPMRGPFKNLALLPFSLPLLGGGGGGGGGGGGFKVSVSKMAAAW------ 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                       A;Accession: S20911
A;Molecule type: DNA
A;Residues: 1-348 <SHA>
A;Cross-references: EMBL:X64397; NID:92832; PIDN:CAA45739.1; PID:92833
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               . 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 35; Mismatches 111; Indels 115;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cuery match 5.9%; Score 85.5; DB 1; Length 348; Best Local Similarity 19.9%; Pred. No. 8.5; Matches 65; Conservation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5.8%; Score 84; DB 2; Length 446; 19.7%; Pred. No. 15; ative 34; Mismatches 110; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SLIDFI--LISMQIVGPSDGSSYILD 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           325 ELADVYDKMVKGEIVG----RYVVD 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Superfamily: hypothetical protein c0103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Experimental source: strain A3(2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 5.8%
Best Local Similarity 19.7%
Matches 52; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              :Genetics:
:Gene: SCOEDB:SC4B5.13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A: Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            68
```

qq

δ

ò qq ò Op ò Ω ò qq ŏ

```
1-764 <MEJ>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Residues: 1-99 <WUL>
                                                                                                                                                                                                                                                                                                                                                                                                  A: Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Accession: A00934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Accession: A19188
                                                                                                                                                                                                                                                                                                                                                                      534675
                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Residues:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   alcohol dehydrogenase (EC 1.1.1.1) 1 - yeast (Kluyveromyces marxianus var. marxianus)
C:Species: Kluyveromyces marxianus var. marxianus. Candida kefyr
C:Species: Kluyveromyces marxianus var. marxianus. Candida kefyr
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 28-Ju1-2000
C:Accession: 532521
R:Ladriere, J.M.; Delcour, J.; Vandenhaute, J.
R:Ladriere, J.M.; Delcour, J.; Vandenhaute, J.
A:Title: Sequence of a gene coding for a cytoplasmic alcohol dehydrogenase from Kluyverc
A:Reference number: 532521; MUID:93250057; PRID:8485163
   GB:AE000513; NID:g6458751; PIDN:AAF10608.1; PID:g645874
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Superiamily: alcohol dehydrogenase: long-chain alcohol dehydrogenase homology (Keywords: alcohol metabolism; metalloprotein: NAD: oxidoreductase; zinc. 29-316/Domain: long-chain alcohol dehydrogenase homology (LADH) (44,67,154/Binding site: zinc, catalytic (Cys, His, Cys) #status predicted 98,101,104,112/Binding site: zinc, noncatalytic (Cys) #status predicted
                                                                                                                                                                                                                                                a)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              159
                                                                                                                                                                                                                                                                                                                                                                                                                              89 ----SVT---TGPWGAVATSAGGEESLKCEDLKVGQYIGKDPKINDATQEPVNGINYT 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      65 LSGSOHSLJUVSENAPASCUFNSAAGSENMTAATLEGSPYA-----------------TA 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            92 KWLNGSCMSCEBCELSNEPNCPKADLSGYTHDGSFQQYATADAVQAARIPKNVDLAEVAP 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 170 FKPISCRNVNGYSYKVAVALSLFLGWLG--AD-RFYLGYPALGILK--FCTVGFCGIGSL 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ę
                                                                                                                                                                                                                                                                                                              38
                                                                                                                                                                                                                                                                                                                                                                   64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A Molecule type: DNA
A; Residues: 1-348 < LAD>
A; Residues: 1-348 < LAD>
A; Cross-treferences: EMBL:X60224; NID:q6822201; PIDN:CAA42785.1; PID:q297908
C; Genetics:
A; Gene: ADH1
C; Superfamily: alcohol dehydrogenase; long-chain alcohol dehydrogenase homol; Keywords: alcohol metabolism; metalloprotein: NAD: oxidoreductase; zinc
F; 29-336/Domain: long-chain alcohol dehydrogenase homology < LADH>
F; 44, 67,154/Binding site: zinc, catalytic (Cys, His, Cys) *status predicted
F; 98,101,104,104,112/Binding site: zinc, noncatalytic (Cys) *status predicted
                                                                                                                                                                                                                                                                                                                                                      17 PIKKLLPVVLLASVLTACGGGTSTPG-----TSTPNTPAVPSSAVAPKLSG---FV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          33 PFKNL---ALLPFSLP1LGGGGSGSGEKVSVSKMAAAWPSGPSAP-EAVTARLVGV1WFV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19 NTRRDG---TGLYPMRGPFKNLALLPFSLPLLGGGGSGSGEKVSVSKMAAAWPSG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     37 NVKYSGVCHTDLHAWOGDWP----LDTKLPLV-GGHEGAGIVVAMGENVTGWEIGDYAGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  152 ILCAGVTVYKALKSAHIKAGDWVAISGACGGLGSLAIQYAKAMGYRVLGIDAGDEKAKLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              116 ----GQYICKDPKINDATQEPVNCTNYTAHVSCFFAPNITCKDSSGNETHFTGNE--VGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      212 KELGGEYFIDFTKTKDMVAEVIEATNGVAHAVINVSVSEAAISTSVLYTRSNGTVVLVGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       83 ----GV-----LWFVSVTTGPWGAVATSAGGEESI,KCEDLKV-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        38; Mismatches 107; Indeis 102;
                                                                                                                                                                                                                                                   .
† †
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    71 ------VTARLV-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5.8%; Score 83; DB 1; Length 348; 26.8%; Pred. No. 14;
                                                                                                                                                                                       DB 2; Length 137,
                                                                                                                                                                                                                                                   48; Indels
                                                                                                                                                                                    5.8%; Score 83; DB 26.5%; Pred. No. 4.9;
                                                                                                                                                                                                                                            16; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  140 AHVS-CFPAPNITCKDSSGNETHFIGN 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          107 VSLSGSYPKASVICINSAGSDILSLGN 133
A; Experimental source: strain Rl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ouery Match
Best Local Similarity 26.8'
Matches 65; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        225 IDFILISMOIVG 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   330 YD-KMVKGQIVG 340
                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                       Best Local Similarity
                                                                                             A; Gene: DR1033
A; Map position: 1
                                                                                                                                                                                                                                                39;
                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ^{\circ}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         q
                                                                                                                                                                                                                                                                                                                                                                   QQ
                                                                                                                                                                                                                                                                                                                                                                                                                              õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   υţ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DD.
```

```
Conference (actor By procurate, C3 procetivator; glytine:rich beta-glycoprocating conference (actor By procurate C3 procetivator; glytine:rich beta-glycoprocating candinates and terrate two species (actor by processing candinates) and terrate two species (actor by processing candinates) and terrate two species (actor by processing candinates) and the candinates (actor by candinates) and (actor by candinates) and (actor by candinates) and (actor by can
```

9

```
57 KVSVSKMAAAWPSGPSAPEAV-TARLVGVLWFVSVTTGPWGAVATSAGGHESLKCEDLKV 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         transferrin-like protein Ttf-1, salt-induced - green alga (Dunaliella salina)
                                                                                                                                                                                                                         C; Species: Dunaliella salina
C; Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999
C; Accession: T10729
R; Fisher, M: Gokhman, I:; Pick, U; Zamir, A.
Submitted to the EMBL Data Library, November 1996
A; Reference number: 217101
A; Accession: T10729
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: mRNA
A; Residues: 1-1274 FFISS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            116 GQYICKDPKINDATQEPVNCTNYTAHVSCFPAPNITCKDSSGNETHFTGNEVGFFKFISC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5.8%; Score 83; DB 2; Length 1274; 22.9%; Pred, No. 61; tive 17; Mismatches 50; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A:Cross-references: EMBL:U77059; NID:g1684791; PID:g1684792
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Search completed: September 26, 2003, 17:26:38 Job time : 48 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Gene: ttfl
C;Superfamily: transferrin repeat homology
    162 AGYCSNPGIPIGTRKV-GSQYRL 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                176 RNVNGYSYKVA 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          666 RDYNGPNLNTA 675
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 30; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        õ
    3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A Pathway: complement alternate pathway
C; Superfamily: complement C2: complement factor H repeat homology; trypsin homology; von
C; Superfamily: complement C2: complement alternate pathway;
C; Superfamily: complement C2: complement alternate pathway;
C; Syponatin: signal sequence fistatus predicted <STG;
F; 26-764/Product: complement factor B #status experimental <MAI>
F; 26-754/Product: complement factor B #status experimental <MAI>
F; 26-754/Product: complement factor H repeat homology <FH3>
F; 103-158/Domain: complement factor H repeat homology <FH3>
F; 105-218/Domain: complement factor H repeat homology <FH3>
F; 105-218/Domain: complement factor H repeat homology <FH3>
F; 260-764/Product: C3/C5 convertase Bb fragment *status experimental <PRF>
F; 268-764/Product: C3/C5 convertase Bb fragment *status experimental <PRF>
F; 268-766/Domain: trypsin homology #status atypical <TRP>
F; 27-75/Domain: trypsin homology #status atypical <TRP>
F; 27-75/Domain: trypsin homology #status atypical <TRP>
F; 27-75/Domain: trypsin homology #status atypical <TRP>
F; 27-76/Domain: trypsin homology #status atypical <TRP>
F; 27-76/Domain: trypsin homology #status atypical <TRP>
F; 27-76/Domain: trypsin homology #status experimental *status experimental <Pre>
F; 256-76/C1eavage site: Arg-Lys (complement factor D) *status experimental 
                                                                                                                                                                                                                                 A.Residues: 16-225, F', 227-259 <MCR>
R.Schwaeble, W.; Luttig, B.; Sokolowski, T.; Estaller, C.; Weiss, E.H.; Meyer zum Buscher Immunobiology 188, 221-232, 1993
A.Title: Human complement factor B: functional properties of a recombinant zymogen of the A.Reference number: 154409; MUID:94041399; PMID:8225386
A.Accession: 154409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mol. Immunol. 30, 1587-1592, 1993
A:Title: Human complement factor B: cDNA cloning, nucleotide sequencing, phenotypic conv
A:Reference number: IS7824; MUID:94067177; PMID:8247029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Map position: 6p21.3-6p21.3
A; Introns: 21/3: 99/3: 346/1: 390/1: 424/1: 470/1: 502/3: 542/1: 593/2; 615/1: 652/3: 65 A; Note: the list of introns may be incomplete
A; Note: gene is located in the major histocompatibility complex, class III region C; Complex: complement factor B initially forms an inactive complex with complement factor C; Cycomplex and inactive complex with complement factor C; Function:
                        A;Title: Internal Homologies of the Ba fragment from human complement component factor
A;Reference number: A44628; MCID:84158524; PMID:6323161
A;Accession: A44628
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Description: Bb is a scrine proteinase; C3/C5 convertase cleaves complement 0.3 alpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A:Cross-references: GB:S67310; NID:9452937; PIDN:AAD13989.1; PID:94261689
R:Horiuchi, T.; Kim, S.; Matsumoto, M.; Watanabe, I.; Fujita, S.; Volanakis, J.E.
Mol. Immunol. 30, 1587-1592, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 SKMAAAWPSG--PSAPEAVIARLVGVLWFVSVITGPWGAVAIS-----AGGEESLKC-- 11C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        56 QALEYVCPSGFYPYPVQTRTCR-----STGSWSTLKTQDOKIVRKAECRAIHCPR 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      111 -EDLKVGQYICKDPKINDATQEPVNC-TNYTAHVSCFPAPNITCKDSS--GNETHFIGNE 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               106 PHDFENGEYWPRSPYYNVSDEISFHCYDGYTLRGSA----NRTCQVNGRWSGQTALCDNG 16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24 GTGLYPMRGPFKNLALLPFSLPLLGGG------GSGSGEKVSV------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 GSNLSP-----OLCLMPFILGLLSGGVTTTPWSLARPQGSCSLEGVEIKGGSFRLLQEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Caps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A)Status: translated from GB/EMBL/DD3J
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Mosidus: 1-31, 'Q', '33-764 <RE2>
A;Cross-rrferences: GB:L15702, NID:g291921; P:DN:AAA16820.1; PID:g291922
C;Comment: 292-Cys has a free sulfhydry!.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5.8%; Score 83; DB 1; Length 764;
24.1%; Pred. No. 34;
tve 21; Mismatchos 71; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: GDB:119726; OMIM:138470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  167 VGFFK----PISCRNVNGYSYKV 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Status: translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 24.1
Matches 49; Conservative
J. 3, 153-157, 1984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: mRNA
A; Residues: 1-764 <RES>
                                                                                                                                                       A; Status: preliminary
                                                                                                                                                                                                 A: Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Accession: 157824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            q
```

34;

Н

us-09-852-100a-2.rsp

```
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
```

OM protein - protein search, using sw model

September 26, 2003, 17:15:17; Search time 23 Seconds (without alignments) 550.008 Million cell updates/sec Run on:

US-09-852-100A-2 1439 1 MHILKGSPNVIPRAHGQKNT.....TRLTRLSITNEFFRKTGLYP 269 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

127863 seqs, 47026705 residues Searched:

127863 Total number of hits satisfying chosen parameters:

Minimum DB seq length: C Maximum DB seq length: 2060000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

SwissProt_41:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	scription	P3428C caenorhabdi		P50257 porphyra pu					Q67288 kluyveromyc		9 homo	myrob	COMO:	::cmo	Sus				8	P27395 j genome po	٠	j genome	P45443 neurospora			Q9y345 homo sapien	-	xeno	OB8799 mus musculu	536.1	026843 methanobact	03303	methanosa	P20241 drosophila
SUMMARIES		1 YKK3_CAEEL	1 VGL2_CVMA5	1 EF1S_PORPU	1 LCT2_MOUSE	1 ADH2_KLUI.A	1 LAMP_RAT	1 Y346_MYCTU	i ADH1_KLUMA	1 CFAB_HUMAN	1 LAMP_HUMAN	1 VG32_BPMD2	1 ENT1_RUMAN	: IBP2_HUMAN	1 LIPP_PIG	: OARI_LYMST	1 ANSP_MYCTU	1 POLG_HRV3	1 AUXI_BOVEN	1 POLG_JAEV1	1 POLG_JAEV5	1 POLG_JAEVJ	DY H(CRS3_	MUB1		YP85	1 AROC_METTH	1 POLG_HRV14	1 IDI2_METMA	1 NRG_DROME
	gth	بع ا	٣.	7	6.0 151	6	σ.	en.	œ.	ω.	۲.	9.	9.	9.	9.	9.	s.	ĸ.	ın.	ı.	.5	٥.	'n.	S.	'n.	S.	5.	s.	'n.	4.	₹.	₹.	₹.	₹.
•	ore	167.5	06	89.5	86.5	85.5	85	83.5	83	83	82.5	80.5	80.5	၁၉	06	90	79.5	79.5	79.5	79.5	79.5	79.5	79.5	79	79	79	78.5	78.5	78.5	7.8	77.5	77.5	77	77
	Result No.		7	3	4	S	œ	7	œ	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29	30	31	32	33

P35999 saccharomyc	09jzg5 neisseria m	P54315 homo sapien	Q9hvt8 pseudomonas	C9erg2 mus musculu	000107 ictalurid h	Q8zf61 yersinia pe	O9z261 mus musculu	P20369 kluyveromyc	P81132 volvox cart	P04480 citrobacter	Q03355 drosophila
PMIP_YEAST	METX_NEIMB	LIP1_HUMAN	GATA_PSEAE	STR3_MOUSE	VG67_HSVI1	WRBA_YERPE	CLD7_MOUSE	ADH1_KLULA	PER2_VOLCA	CEA_CITFR	PER_DROSI
ч	٦	Н	٦	٦	Н	٦	-	П	-	-	-
772	379	467	484	796	1556	199	21:	350	484	592	929
5.3	5.3	5.3	5.3	5.3	5.3	5.2	5.5	5.2	5.2	5.2	5.2
5.5	76	16	97	76	76	75.5	75.5	75.5	75.5	75.5	75.5
76											

ALIGNMENTS

YKK3_CAEEE 11 YKK3_CAEEE 12 YKK3_CAEEE 13 YKK3_CAEEE 14

```
435
530
625
625
6657
668
737
754
893
11180
11209
1225
                                                                                                                                                                                                                                                                                                             Similarity
59; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Porphyra purpurea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BIOSYNTHESIS.
                                                                                          688
737
754
893
11180
11209
1225
11246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=2787;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EF1S_PORPU
P50257:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota;
                                                      CARBOHYD
CARBOHYD
                                                                                          CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                      CARBOHYD
                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                CARBOHYD
                                                                                                                                               CARBCHYD
                                                                                                                                                                    CARBOHYD
                                                                                                                                                                                   CARBOHYD
                                                                                                                                                                                                      CARBOHYD
                                                                                                                                                                                                                       CARBOHYD
                                                                                                                                                                                                                                                         SEQUENCE
                      CARBOHYD
                                         CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 pha).
                                                                                                                                                                                                                                                                                                                Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EF1S_PORPU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TEF-S
                                                                                                                                                                                                                                                                                                              Best Loca
Matches
 8
                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    끉
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ζ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation; the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in ro way modified and this statement is not removed. Usage by and for commercial entities requires a license afterement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                              5
                                                                                                                                                                                                    465
                                                                                                                                                                  -----K 124
                                                                                                                                                                                                                                        125 INDATQEPVNCTNYTAHVSCFPAPNITCKDSSGNETHFTGNEVGFFKPISCRNVNGYSYK 184
                                                                                                                                                                                                                                                                     466 MGGYRAEDVEFTN----VKCRVLPCIEC---HGPRT------FTKSTPCIIYNGHYFL 510
                                                                                                                                                                                                                                                                                                             185 VAVALSLFLGWLGADRFYLGYPALGLLKFCTVGFCGIGSLIDFILISMQIVGPSDGSSY 243
                                                                                                                                                                                                                                                                                                                                     SII TTLLYSIFLGVVAVDRFCLGYSAMAVGKLMTLGGFGIWWIVDIFLI.VIGVLGPADDSSW 569
                                                                                                                                                                                                    415 VSTNPLGPV-----VECRFLENSFILCEDPVPLYGPGOTGOOPANESFRNEGKCLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Luytjes W., Sturman L.S., Bredenbeek P.J., Charite J., van der Zeijst B.A.M., Horzinek M.C., Spaan W.J.M.;
*Primary structure of the glycoprotein E2 of coronavirus MHV-A59 and identification of the trypsin cleavage site.";
virology 161:479-487(1987).
-i. FUNCTION: THE PEPLOMER PROTEIN MEDIATES THE BINDING OF VIRIONS
                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   S.
Murine coronavirus (strain AS9) (MHV-AS9) (Murine hepatitis virus).
Viruses: SSRNA positive-strand viruses, no DNA stage: Nidovirales:
Coronaviridae: Coronavirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22 glycoprotein precursor (Spike glycoprotein) (Peplomer protein) (Contains: Spike protein S1 (90B); Spike protei: S2 (90A)].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TO THE HOST CELL RECEPTOR AND IS INVOLVED IN MEMBRANE FUSION AND IN SYNCYTUM FORMATION.
--- SUBCELLULAR LOCATION: Type I membrane protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
                                                                                                                                49.
                                                                                            1: Length 573;
                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Glycoprotein; Envelope protein; Transmembrane; Signal.
SIGNAL
                                                      64299 MW; BA437D93C898B9AC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CYTOPLASMIC (POTENTIAL)
   GTP (BY SIMILARILY).
                  GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
                                                                                                                                                                    90 VIIGPWGAVAISAGGEESLKCEDLKVGQYICKDP----
                                                                                       Score 167.5; DB : Pred. No. 2.8e-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (Rel. 11, Created)
(Rel. 33, Last sequence update)
(Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EZ GLYCOPROTEIN.
SPIKE PROTEIN SI
SPIKE PROTEIN SZ
                                                                                                           ; Pred. No. 2.8e
23; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT; 1324 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-88072088; PubMed=2825419;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR002552; Corona_S2.
                                                                                          11.6%; 27.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; M18379; AAA46455.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF01601; Corona_S2;
                                                                                                                                50; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1324
1324
1265
1286
1324
1304
1304
1303
31
69
115
246
573 AA;
                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID-11142;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17
17
718
17
1266
1287
1287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31
60
192
357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUL-1989 (
01-FEB-1996 (
15-SEP-2003 (
E2 9lycoprote
                                                                                                                                                                                                                                                                                                                                                                                                                                      VGL2_CVMA5
P11224;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CARBOHYD
CARBOHYD
CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
TRANSMEM
DOMAIN
DOMAIN
                  NP_BIND
NP_BIND
SEQUENCE
                                                                                            Query Match
 NP_BIND
                                                                                                               Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 2
VGL2_CVMA5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CHAIN
                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                          A PART TETTE TETTE
                                                                                                                                                                                                    Ďρ
                                                                                                                                                                                                                                                                         qc
                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                             ò
 FT
FT
SO
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation \cdot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       74 PEAVTARLVGVLWFVSVTTGPWGAVATSAGGEESLKCEDLKVGQY-ICKDPKINDATQEP 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            133 VNCTNYTAHVSCFPAPNITCKDSSGNETHFTGNE-VGFF----KPISCRNVNGYSYKVAV 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----YTDCKPNTN-----GNKLIGFWHTDVKPPICVLKRNFTLNVNA 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  188 ALSLFLGWLGADRFYLGY----PALGLLKFCTVGFCGIGSLIDFILLISMQIVGPSDGSSYI 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       200 DAFYFHFYQHGGIFYAYYADKPSATIFLFSVY----IGDILIOYYVLPFICNPTAGSIFA 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            124 PIIVIGSLEGYISY-TVVIEPYNGVIMAS------VCQYTICQLP------ 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25 TGLYPMRG-PFKNLALLP-----FSLPLLGGGGSGSGSGKVSVSKMAAAWPSGPSA-- 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rhodophyta; Bangiophyceae; Bangiales; Bangiaceae; Porphyra
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BORING, FILAMENTOUS PHASE.
SIMILARITY: BELONGS TO THE GTP-BINDING ELONGATION FACTOR FAMILY
EF-TU/FF-1A SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBCELLULAR LOCATION: Cytoplasmic.
DEVELOPMENTAL STAGE: EXPRESSED ONLY IN THE SPOROPHYTE, A SHELL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-Avonport;
MEDLINE-96309386; FubMed-8704161;
Liu Q.Y., Baldauf S.L., Reith M.E.;
Liu Qation fator I alpha genes of the red alga Porphyra purpurea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               O.F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0:-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Elongation factor 1-alpha S (EF-1-alpha S) (Sporcphyte-specific
                                                                                                                                                                                 (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     70:
                                                                                                                                  POTENTIAL)
                                                                                                                                                                                                                                                   (PCTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                   (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                  (POTENTIAL)
                                                                                                                                                                                                                                                                                                  (POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  include a novel, developmentally specialized variant. Flant Mol. Biol. 31.77-85(1996).
-!- FUNCTION: THE PROPERTE THE GTP-DEPENDENT BINDING AMINOACYL-IRNA TO THE A-SITE OF RIBOSOMES DURING PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6.3%; Score 90; DB 1; Length 1324; 23.6%; Pred. No. 5.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               94; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-LINKED (GLCNAC...) (POTIN-LINKED (GLCNAC..
N-LINKED GLCNAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           515 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         146019 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       245 IDYYGTRLTR 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        256 PRYWVTPLVK 265
```

3

```
ADH2_KLULA
                                                                                                                                                                                                                                                                                                                                                                                                                       VARIANT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NADH
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                       VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P49383:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADH2_KLULA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  â
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ŝ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             S
           use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                        ÷
                                                                                                                                                                                                                                                                                                                                                                      261 PLRLPLQDVYKIGGIGTVPVGRVETGILKAGMQVTFEPAGKAAVEVKSVEM-----HH 313
                                                                                                                                                                                                                                                                                                                                                                                              91 TTGPWGAVATSAGGEESLKCEDLKVGQYICKDPK------INDATQEPVNCTN-- 137
                                                                                                                                                                                                                                                                                                                                                                                                             41 PFSLPL-----LGGGGSGSGEKVSVSKMAAAW-----PSGPSAPEAVTARLVGVLWFVSV 9U
  restrictions on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Shukunami C., Kondo J., Wakai H., Takahashi K., Inoue H., Kamizono A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Molecular cloning of mouse and bovine chondromodulin-II cDNAs and the growth-promoting actions of bovine recombinant protein.";
J. Biochem. 125:48-442(1999).
-i. FUNCTION: Has a neutrophil chemotactic activity. Also a positive
                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Yamagoe S., Watanabe T., Mizuno S., Suzuki K.;
The mouse Lect2 gene: cloning of cDNA and genomic DNA, structural
characterization and chromosomal localization.";
Gene 216:171-176(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus (Mouse).
Eukaryota: Metazoa; Chordata; Cramiata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LCT2_MOUSE STANDARD: PRT: 151 AA.
088803: 088804: Q90MN: Q92337;
088803: O88804: Q90MN: Q92337;
15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Leukocyte cell-derived chemotaxin 2 precursor (Chondromodulin II)
                                                                                                                                                                                                                                                                                                                       37;
                                                                                                                                                                                                                                                                                                 DB 1; Length 515;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. (ISOFORMS 1 AND 2), AND VARIANT VAL-129
                                                                                                                                                                                                                                                                                                                       56; Indels
                                                                                            InterPro; IPR004539; EFL_alpha.
InterPro; IPR004539; EF_GTPbind.
InterPro; IPR004160; EFTU_Cterm.
InterPro; IPR004161; EFTU_D2.
Pfam; PF00109; GTP_EFTU; 1.
Pfam; PF03144; GTP_EFTU, D2: 1.
Pfam; PF03143; GTP_EFTU_D2: 1.
PTGFRMS; TIGR00483; EF-L_alpha; 1.
PROSITE; PS00301; EFACTOR_GTP; 1.
                                                                                                                                                                                                                                                                         EBAC3F4029F62350 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. (ISOFORM 1).
STRAIN-Swiss Webster / NIH: TISSUE-Embryc, and Liver:
MEDLINE-99160594; PubMed-10050329;
 There are no
                                                                                                                                                                                                                                   GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                              138 -----YTAHVSCFPAPNITCKDSSGNETH 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     373 TPVLDCHTAHIACKFASILSKKDKRGKQTH 402
                                                                                                                                                                                                                                                                                                           Pred. No. 2.1;
                                                                                                                                                                                                                                                                                                                       20; Mismatches
                                                                                                                                                                                                                                                                                                6.2%; Score 89.5; 24.7%; Pred. No. 2.
the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-BALB/c; TISSUE=Liver;
MEDLINE=98382586; Pubmed-9714793;
                                                                                                                                                                                                                                                                         56648 MW;
                                                                       EMBL; U08841; AAA61796.1; -. HSSP; P07157; 1AIP.
                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                21
95
154
                                                                                                                                                                                                                                                         151
515 AA;
                                                                                                                                                                                                                                                                                                         l Similarity
37; Conserv
                                                                                                                                                                                                                         Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hiraki Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (ChM-II).
                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                               NP_BIND
NP_BIND
                                                                                                                                                                                                                                     NP_BIND
                                                                                                                                                                                                                                                                                                            Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LCT2_MOUSE
 a
                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     q
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bicinformatics and the EMBL outstation. the European Bicinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             78 TARLVGVLWFVSVTTGPWGAVAISAGGEESLKCEDLKVGQYICKDPKINDATQEPVNCTN 13"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5.7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FCVKIFYIKPIKYKGSIKKGEKLGTLLPLQKIYPGIQSHVH
VENCDSSDPTAYL -> QRLQAHTTILNVFTCYWDKIQIPR
PIRFLCQNFLH (in isoform 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                138 YTAHVSCFPAPNITCKDSSGNETHFTGNEVGFFKPISCRNV------NGYSYKV 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ---H---HPGVDVLCSDGSVVYAPFTGKIVGQEKPYRNKNAINDGIRLSGRGFCVKI 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-CBS 2359 / IFO 1267 / NRRL Y-1140;
MEDLINE-92269769; PubMed=1588917;
Shain D.H., Salvadore C., Denis C.L.;
"Evolution of the alcohol dehydrogenase (ADH) genes in yeast:
characterization of a fourth ADH in Kluyveromyces lactis.";
Mol. Gen. Genet. 232:479-488(1992).
-!- CATALYTIC ACTIVITY: An alcohol + NAD(+) - an aldehyde or ketone +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 TTILISAALLSSALAGPWANICASKSSNEIRTCDSYGCGOYSAO-----RIOR-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27; Gaps
                                                                                                                                                                                                                                                                      -:- IISSUE SPECIFICITY: Highly expressed in liver and weakly in testis. Not expressed in heart, brain, splee:, lung, skeletaimuscle and kidney.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LEUKOCYTE CELL-DERIVED CHEMOTAXIN 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kluyveromyces lactis (Yeast).
Eŭkaryota: Fungi: Ascomycota; Saccharomycetina: Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Kluyveromyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6.0%; Score 86.5; DB 1; Length 151; 24.8%; Pred. No. 0.89;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18AF444046B7AE8E CRC64
                                                                                                          Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /FTId-VSP_003051.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence updatc)
15-FEP-2003 (Rel. 42, Last annotation update)
Alcohol dehydrogenase II (EC 1.1.1.1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      348 AA
regulator of chondrocyte proliferation.
SUBCELLULAR LOCATION: Secreted.
ALTERNATIVE PRODUCIS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chemotaxis; Signal; Alternative splicing.
SIGNAL 1 18 BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9; Mismatches
                                                                                                                                                                      IsoId=088803-1; Sequence-Displayed;
Name=2; Synonyms-LECI2Q;
IsoId=088803-2; Sequence-VSP_003051;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                   Event-Alternative splicing;
Name=1; Synonyms-LECT2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL: AB009687; BAA33383.1; -. EMBL: AB009689; BAA33384.1; -. EMBL: AB009689; BAA33385.1; -. EMBL: ABC09689; BAA33386.1; -. EMBL: AF035161; AAF13302.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   129 129
151 AA; 16405 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MGD; MGI:1278342; Lect2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
ses 29; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID-28985;
```

J

```
SEQUENCE FROM N.A., AND SEQUENCE OF 29-49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMA IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CHAIN
     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ó
                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL cutstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----- 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               166 EUGFFKPISCRNVNGYSYKVAVALSLFLGWLG--AD-RFYLGYPALGLLKFCTVGFCGLG 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                266 VVLVGLPRDAKCKSDVFTQVVKSVSIVGSYVGNRADTREALDFFARGLV-HAPIKTVGLS 324
                                                                                                                                                                                                                                                                                                                                                                                                                                         67
                                                                                                                                                                                                                                                                                                                                                                                                                                                               91
                                                                                                                                                                                                                                                                                                                                                                                                                                         19 NTRRDG---TGLYPMRGPFKNLALLPFSLPELLGGGGSGSGGEKVSVSKMAAAW-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                         116 ----GQYICKDPKINDAIQEPVNCTNYTAH-----VSCFPAPNITCKDSSGNETHFTGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             92 KWLNGSCMSCEYCELSNESNCPDADLSGYTHDGSFQQYATADAVQAARIPKGTDJAEVAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutoleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                            -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
                                                                                                                                                                                                                                                       Oxidoreductase; Zinci Metal-binding; NAD; Multigene tamily.

METAL 44 44 ZINC 1 (CATALYTIC) (HY SIMILARITY).

METAL 67 ZINC 1 (CATALYTIC) (BY SIMILARITY).

METAL 101 101 ZINC 2 (BY SIMILARITY).

METAL 112 104 ZINC 2 (BY SIMILARITY).

METAL 112 114 ZINC 2 (BY SIMILARITY).

METAL 112 114 ZINC 2 (BY SIMILARITY).

METAL 115 ZINC 2 (BY SIMILARITY).

METAL 115 ZINC 2 (BY SIMILARITY).

METAL 115 ZINC 2 (BY SIMILARITY).

METAL 116 ZINC 3 (CATALYTIC) (BY SIMILARITY).

SEQUENCE 348 AA, 37097 MM; F3B64AEIF520689C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                               35; Mismatches 111; Indels 115;
                                                                                                                                                                                                                                                                                                                                                                                       DB 1; Length 348;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Limbic system-associated membrane protein precursor (LSAMP)
COFACTOR: Binds 2 zinc ions per subunit (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         79 ARLVGV-----LWFVSVTTGPWGAVATSAGGEESLKCEDLKV-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                      5.9%; Score 85.5; Di
19.9%; Pred. No. 2.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      338 AA
                SUBUNIT: Homotetramer (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               223 SLIDFI--LISMQIVGPSDGSSYIID 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       325 ELADVYDKMVKGEIVG----RYVVU 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT:
                                                                                                                                                                                                        InterPro; IPR002328; ADH_Zinc.
InterPro; IPR002085; Adh_Zn_family.
Pfam; PF00107; ADH_Zinc.N; I.
PROSITE; PS00059; ADH_ZINC; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LAMP_RAT STANDARD; F 062813; O1-NOV-1997 (Rel. 35, Last sequent) 01-NOV-1997 (Rel. 35, Last sequent) 15-SEP-2003 (Rel. 42, Last annotation)
                                                                                                                                                                                EMBL; X64397; CAA45739.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                             S20911; S20911
                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID-10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LSAMP OR LAMP.
                                                                                                                                                                                                                                                                                                                                                                                                               65;
                                                     family.
                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local 9
                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LAMP_RAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
  q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstain the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               101 SAGGEESLKCEDLKVG----QYICKDPKINDATQEPVNCTNYTAHVSCFPAPNITCKDSS 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         157 GNETHFTGNEVG------FFKPISCRNVNGYSYKVAVALSLFLGWLGADRFYLGYPALG 209
                                                                                                            MEDLINE-95574785; PubMed-7646886;
Pimenta A.F., Zhukareva V., Barbe M.F., Reinoso B.S., Grimley C.,
Henzell W., Fischer I., Levitt P.;
"The limbic system-associated membrane protein is an ig superfamily
member that mediates selective neuronal growth and axon targeting.";
Neuron 15:287-297(1995).
                                                                                                                                                                                                                                                                                                                               HYPOTHALAMUS, PERIRHINAL CORTEX, AMYGDALA AND MEDIAL THALAMIC
                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. IGLON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REMOVED IN MATURE FORM (POIENTIAL).
IG-LIKE C2-TYPE 1.
IG-LIKE C2-TYPE 2.
IG-LIKE C2-TYPE 3.
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE: PS50835; IG_LIKE: 3.
Immunoglobulin domain; Cell adhesion; Glycoprotein; GPI-anchor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         32;
                                                                                                                                                                                                                                                                                                                                                                                       SUBFAMILY. SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SYSTEM-ASSOCIATED MEMBRANE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5.9%; Score 85; DB 1; Length 338; 27.7%; Pred. No. 3.1; tive 15; Mismatches 47; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0B76AFDD68A39BB6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POTENTIAL
N-LINKED (GLONAC...) (
N-LINKED (GLCNAC...) (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GPI-ANCHOR (POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  - I: - I: - - I:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LIMBIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             37324 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; J31554; AAA86120.1; -. InterPro; IPR007110; Ig-11ke. InterPro; IPR003598; Ig_c2. InterPro; IPR003006; Ig_MHC. Pfam; PF00047; ig; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SMART; SM00408; IGc2; 2.
PROSITE: PS50835; IG_LIKE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28
315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                300
315
315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       122
214
304
111
197
290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      40
66
136
148
279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  <del>...</del>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    40
666
1366
279
287
380
315
315
38 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
Matches 36; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Repeat; Signal
                                                                                                                                                                                                                                                                                                                                                       REGION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CARBOHYD
```

```
ADHI_KLUMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             family
                                                 TRANSMEM
TRANSMEM
TRANSMEM
                                                                                                                                                                       TRANSMEM
TRANSMEM
                                                                                                                                                                                                                      SEQUENCE
                                                                                                                     TRANSMEM
                                                                                                                                                   TRANSMEM
                           FRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADEL_KLUMA
                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ô
                                                                                                                                                                                                                                                                                                                                                                                                                  f
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Baloniformatics and the FSML outstation. The European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
286 GNYTCVAANKLGVTNASLVLFRPGSVRGING-SISLAVPL----WL-----LM 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDINE-9895987: PubMed=9634230;

Cole S.T., Brosch R., Parkill J., Garnier J., Churcher C., Harris C.,

Cole S.T., Brosch R., Parkill J., Garnier J., Churcher C., Harris C.,

Cordon S.V., Bigiameir K., Gas S., Barry C.E., Ill, Tekdia F.,

Badcock K., Basham D., Brown D., Chillingworth T., Cornor R.,

Davies R., Devlin K., Feltwell T., Gentles S., Hamin N., Holroyd S.,

Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,

Oliver S., Osborne J., Quall M., Rajandream M.A., Royers J.,

Rutter S., Seeger K., Whitchcad S., Squarcs R.,

Sulston J.E., Taylor K., Whitchcad S., Barrell B.G.;

Deciphering the biology of Mycobacterium tuberchlosis from the

Complete genome sequence.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fleischmann R.D., Alland D., Eisen J.A., Carpenter J., White O., Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E., Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.J. Belcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hypothetical protein; Transport; Amino-acid transport; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'Whole genome comparison of Mycobacterium tuberculosis clinical and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                laboratory strains...
Submitted (APR-2001) to the EMBL/GenBank/2DBJ databases.
FUNCTION: PROBABLE AMINO-ACID OR METABOLITE TRANSPORT PROTEIN...
-: SUBCELLULAR LOCATION: Integral membrane protein (Potential)...
-: SIMILARITY: Belongs to the amino acid permease family.
                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium:
                                                                                                                                                                                                                                                            15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Pypochetical transport protein RV0346c.
RV0346C OR MT0361 OR MTCY13E10.06C.
                                                                                                                                                                                                                    487 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00324; aa_permeases; 1.
PROSITE; PS00218; AMINO_ACID_PERMEASE_1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POTENTIAL. POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TubercuList; Rv0346c; -
InterPro; IPR002203; AA/rel_permeasel.
InterPro; IPR004840; AAc_permease.
InterPro; IPR304841; Permease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL, AE006942; AAK44583.1; -. PIR, C70574, C70574.
TIGR; MT0361; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; 295324; CAB08578.1; -.
                                                                                                                                                                                                                                                                                                                                                                                           Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=CDC 1551 / Oshkosh;
                                                                                                                                                                                                                      STANDARD;
                                                 210 LLKFCTVGFC 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    46
70
118
                                                                                            329 ASLFCLLSKC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=1773;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-H37Rv;
                                                                                                                                                                                                                 Y346_MYCTU
006297;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bishai W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TRANSMEM
                                                                                                                                                                                             Y346_MYCTU
                                                                                                                                                                                                                    THE REPORT OF THE PROPERTY OF 
                                                 ò
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation. The European Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                     159 ETHFTGNEVGFFKPISCRNVNGYSYKVAVALSLFLGWLGADRFYLGYPALGLLKFCTVGF 218
                                                                                                                                                                                                                                                                                                                                                                                                                                       61
                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; X60224: CAA...
EMBL; X60224: CAA...
EMBL; X60224: CAA...

PIR: S32521: 832521.

R InterPro; IPR0022088: ADH_zinc.

DR Pfon: PF00107; ADH_zinc_N: 1.

DR PROSITE; PS00059: ADH_ZiNC: 1.

DR PROSITE; PS00059: ADH_ZINC: 1.

DR PROSITE; PS00059: ADH_ZINC: 1.

THETAL 44 21NC 1 (CATALYICC) (BY SIMILARITY).

FT METAL 67 67 2INC 1 (CATALYICC) (BY SIMILARITY).

2INC 2 (BY SIMILARITY).

2INC 2 (BY SIMILARITY).

2INC 2 (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -:- SUBCELLUIAR LOCATION: Cytoplasmic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ladriere J.M., Delcour J., Vandenhaute J.;
"Sequence of a gene coding for a cytopiasmic alcohol dehydrogenase from Kluyveromyces marxianus ATCC 12424.";
Hiochim, Biophys. Acta 1173:99-101(1993).
-:- CATALYIIC ACTIVITY: An alcohol + NAD(+) = an aldehyde or ketone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kluyveromyces marxianus (Yeast) (Kluyveromyces fragilis).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                     19;
                                                                                                                                                                                                                                                                                5.8%; Score 83.5; DB 1; Length 487; 26.5%; Pred. No. 6.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- COFACTOR: Binds 2 zinc ions per subunit (By similarity)
                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       219 CGIGSLIDFILISMQIVG-----PSDGS--SYIIDYYGIRI, 252
                                                                                                                                                                                                         POTENTIAL.
3572502DB6ACD987 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CGI-----FVFLILRALGELVLHRPSSGSFVSYAREFYGEKV 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Saccharomycetales; Saccharomycetaceae; Kluyveromyces.
                                                                                                                                                                                                                                                                                                                                     70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-FEB-1395 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                     16; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     348 AA
                     POTENTIAL
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
                                                                                                                                                                                 POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Alcohol dehydrogenase 1 (EC 1.1.1.1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN~ATCC 12424;
MEDLINE=93250057; PubMed=8485163;
                                                                                                                                                                                                                                52194 MW:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -! - SUBUNIT: Homotetramer.
                                                                                                                                                                                                                                                                                                                                     27; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
153
183
234
276
310
381
434
                                                                                                                                                                            414 4
440 4
487 AA;
                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID-4911;
```

```
SEQUENCE OF 16-259 FROM N.A.
                                                                                                                                                 SEQUENCE FROM N.A.
     Volanakis J.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lokki M.-L.;
                                                                                                                                                            IISSUE-Cclon
                              prenotypic
     272 PRDAOCK - SDVFNQVVKSISIVGSYVGNRADTREALDFFSRGLVKAPIKILGLSELASV 329
                                                                                                                                                                                                            152 ILCAGVIVYKALKSAHIKAGDWVAISGACGGLGSLAIQYAKAMGYRVLGIDAGDEKAKLF 211
                                                                                                                                                                                                                                             ----GQYICKDPKINDATQEPVNCTNYTAHVSCFPAPNITCKDSSGNETHFIGNE--VGF 169
                                                                                                                                                                                                                                                                   212 KELGGEYFIDFTKTKDMVAEVIEATNGVAHAVINVSVSEAAISTSVLYTRSNGTVVLVGL 271
                                                                                                                                                                                                                                                                                           170 FKPISCRNVNGYSYKVAVALSLFLGWLG--AD-RFYLGYPALGLLK--FCTVGFCGIGSL 224
                                                                                                                                                                      92 KWLNGSCMSCEECELSNEPNCPKADLSGYTHDGSFQQYATADAVQAARIPKNVDLAEVAP 151
                                                                                                  70
                                                                                                                                                 28
                                                                                                                       NVKYSGVCHTDLHAWQGDWP----LDTKLPLV-GGHEGAGIVVAMGENVTGWEIGDYAGI
                                                                                                 19 NTRRDG----TGLYPMRGPFKNLALLPFSLPLLGGGGSGSGSKVSVSKMAAAWPSG----
                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Davrinche C., Abbal M., Clerc A.;
"Molecular characterization of human complement factor B subtypes.";
Immunogenetics 32:309-312(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                            CFAB HUMAN STANDARD; PRI; 764 AA.

20.0751; 0.15006: 0.29944: 0.29644: 0.968195; 0.98752.

21.070-1998 (Rel. 0). Created)
01-0CT-1994 (Rel. 30, Last sequence update)
COMPLEMENT 142, Last annocation update)
COMPLEMENT factor B precursor (EC 3.4.21.47) (C3/C5 convertase)
(Properdin factor B) (Glycine-rich beta giycoprotein) (GBG) (PBF2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Schwaeble W., Luettig B., Sokolowski T., Estaller C., Weiss E.H., Meyer Zum Bueschenfelde K.-H., Whaley K., Dippold W., "Human complement factor B: functional properties of a recombinant zymogen of the alternative activation pathway convertase.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
               54 ZINC 1 (CATALYTIC) (BY SIMILARITY).
37158 MW: A75D2EBE82E355BD CRC64;
                                                                         107; Indels 102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mejia J.E., Jahn I., de la Salle H., Hauptmann G.:
"Human factor B. Complete cDNA sequence of the RF*S allele.";
                                                  5.8%; Score 83; DB 1; Length 346;
                                                                                                                                                                                              ----GV-----LWFVSVTTGPWGAVATSAGGEESLKCEDLKV----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Horiuchi T., Kim S., Matsumoto M., Watanabe 1., Fujita
  ZINC 2 (BY SIMILARITY).
ZINC 1 (CATALYTIC) (BY
                                                               Pred. No. 4.9;
                                                                       38; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (1)
SEQUENCE FROM N.A. (ALLELES S: FA AND FB).
MEDLINE-91065702; Pubmed-2249879;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=94041399; PubMed=8225386;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-94067177; Pubmed-8247029;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=94237735; PubMed=8181962;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mmunobiology 188:221-232(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. (ALLELE S).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. (ALLELE S).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. (ALLELE S)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hum. Immunol. 39:49-53(1994).
                                                            llarity 20.8%;
Conservative 3
                                                                                                                                                                                                                                                                                                                                                                 330 YE-KMVKGQIVG 340
                                                                                                                                                                                                                                                                                                                                          225 IDFILISMQIVG 236
112 1
154 1
348 AA;
                                                            L Similarity
65; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE-Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE-Liver
                                                                                                                       37
                                                                                                                                               7.1
                                                                                                                                                                                                                                             116
                                                                                                                                                                                             83
                          SEQUENCE
                                                  Query Match
                                                               Best Local
               METAL
                                                                                                                                                                                                                                                                                                                                                                                                                 CFAB_HUMAN
                                                                          Matches
  FT
                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                       g
                                                                                                                                               ò
                                                                                                                                                                     q
                                                                                                                                                                                             ò
                                                                                                                                                                                                                   qq
                                                                                                                                                                                                                                             δ
                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                  q
                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                 g
```

```
Krausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Krausberg R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul M.J., Usdin T.B., Tonaldon M.F., Caraninci P., Prange C.,
A. Racha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
A. Richards S., Worley K.C., Hale S., Garninci P., Frange C.,
A. Nilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
A. Vilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
A. Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
A. Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
A. Butterfield Y.S.N., Krzywinski M.T., Skalska U., Smailus D.E.,
B. Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
T. "Generation and initial analysis of more than 15,000 full-iength
Human complement factor B: cDNA cloning, nucleotide sequencing, phenotypic conversion by site-directed mutagenesis and expression."; wol. Immunol, 30:1587-1592(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Molecular cloning and characterization of the gene coding for human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Amino acid sequence of the Bb fragment from complement Factor B. Sequence of the major cyanogen bromide-cleavage peptide (CB-II) and completion of the sequence of the Bb fragment.";
Blochem. J. 209:61-70(1983).
                                                                                                                                                                 SEQUENCE FROM N.A. Rower L., Dankers. C., Ahear: M.E., Banka A., Swartzell S., Smith T.M., Spies T., Hood L., "Sequence determination of 300 kilobases of the human class III MHC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 467-595 AND 752-764 FROM N.A. MEDLINE-83039428; PubMed-6957884; Woods D.E., Markham A.F., Ricker A.T., Goldberger G., Colten H.R.; Isolation of cDNA clones for the human complement protein factor E a class III major histocompatibility complex gene product."; Proc. Natl. Acad. Sci. U.S.A. 79:5661-5665(1982).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 26-764, PARTIAL SEQUENCE FROM N.A., AND CARBOHYDRATES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Complete primary structure for the zymogen of human complement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ξ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. (ISOFORM 2).
Jatinen T., Kanerva J., Poutanen K.E., Saarinen-Pihkala U.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Expression and alternative splicing of human factor B gene leukemic mononuclear cells."; Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                              Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   D.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement protein factor B.";
Proc. Natl. Acad. Sci. U.S.A. 80:4464-4468(1983).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=84161997; PubMed-6546754; Moods Mole J.E., Anderson J.K., Davison E.A., Woods
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    factor B.";
.. Biol. Chem. 259:3407-3412(1984)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-22388257; PubMed=12477932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 260-764.
MEDLINE~83204002; PubMed=6342610;
Christie D.L., Gagnon J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 339-764 FROM N.A.
MEDLINE-83273641; PubMed-6308626;
Campbell R.D., Porter R.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            human and mouse cDNA sequences.
```

```
Socal Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBFAMILY
   MIM; 138470;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LAMP_HUMAN
                                                                                                                                                                                                                                                               Cuery Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 10
LAMP_HUMAN
                                                                                                                                                                                                                                                                                             4a tches
   ä
                                                                                                                                                                                                                                                                                                                                                                                    ð
                                                                                                                                                                                                                                                                                                                                                                                                                   de
                                                                                                                                                                                                                                                                                                                                                                                                                                                 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBH. Outstation the European Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.cn/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                              MEDLINE-91174758; PubMed-200691;
Niemann M.A., Bhown A.S., Miller E.J.;
Niemann M.A., Bhown A.S., Miller E.J.;
Niemann M.A., Bhown A.S., Miller E.J.;
Substitution of stress of glycation of human complement factor H.";
Biochem. J. 274:473-480(191).
-!- FUNCTION: FACTOR B WHICH IS PART OF THE ALTERNATE PATHWAY OF THE COMPLEMENT SYSTEM IS CLEAVED BY FACTOR D INTO 2 FRAGMENTS: SA AND BB. ASERINE PROTEASE; THEN COMBINES WITH COMPLEMENT FACTOR 35 TO GENERALE THE G.3 OR C.S. CONVERTASE. IT HAS ALSO SEEN IMPLICATED IN PROLIFERATION AND DIFFERENTIATION OF PREACTIVATED B
                                                                                                                                                                                                                                                                                                                                                                   LYMPHOCYTES, RAPID SPREADING OF PERIDHERAL BLOOD MONOCYTES, STIMULATION OF LYMPHOCYTE BLASTOGENESIS AND LYSIS OF ERYTHROCYTES.
BA INHIBITS THE PROLIFERATION OF PREACTIVATED B LYMPHOCYTES.
CATALYTIC ACTIVITY: Cleaves C3 in the alpha-chain to yield C3a and C3b. Cleaves C5 in the alpha-chain to yield C3b and c3b. Cleaves C5 in the alpha-chain to yield C5b. Both cleaves Lake place at the C-terminal of an arginine residue.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wu L.C., Morley B.J., Campbell R.D.; "Cell-specific expression of the huma: complement protein factor B gene: evidence for the role of two distinct 5'-flanking elements.";
                               Internal homologies of the Ba fragment from human complement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Event-Alternative splicing: Named isoforms-2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY SI. -!- SIMILARITY: Contains 3 Sushi (SCR) domains. -!- SIMILARITY: Contains 1 VMFA domain.
                                            component Factor B, a class III MHC antigen.";
EMBO J. 3:153-157(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IsoId-P00751-1; Sequence-Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      J00125; -; NOT_ANNOTATED_CDS. J00126; AAA36226.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   J00185; AAA36219.1; ALT_SEQ. J00186; AAA36220.1;
                                                                                                                        MEDLINE-87102880; PubMcd-3643061;
 MEDLINE-84158524; PubMed-6323161;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AF019413; AAB67977.1; -. BC004143; AAH04143.1; -. BC007990; AAH07990.1; -. AF349679; AAK30167.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 S67310; AAD13989.1; -. L15702; AAA16820.1; -. X00284; CAA25077.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAA36220.1; -.
AAA59625.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; X72875; CAA51389.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SWISS-2DPAGE; P00751; HUMAN.
Siena-2DPAGE; P00751;
                   Morley B.J., Campbell R.D.
                                                                                          SEQUENCE OF 1-99 FRCM N.A. TISSUE-Blood;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          K01566; AAA36225.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASS-III PROTEIN.
                                                                                                                                                                                    Cell 48:331-342(1987)
                                                                                                                                                                                                                   GLYCATION OF LYS-291.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genew; HGNC:1037; BF
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Monomer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P20231; 1AAO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 S34075; BBHU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 S01.196;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    M15082;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBCNIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Name=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEROPS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL;
EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SMBL;
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 SKMAAAWPSG--PSAPEAVTARLVGVLWFVSVTTGFWGAVATS-----AGGEESLKC-- 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           56 QALEYVCPSGFYPYPVQIRICR-----SIGSWSILKTQUQKIVRKAECRAIHCPR 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            111 -EDLKVGQYICKDPKINDAIQEPVNC-TNYTAHVSCFPAPNITCKDSS--GNETHFIGNE 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          106 PHDFENGEYWPRSPYYNVSDEISFHCYDGYTLRGSA----NRTCQVNGRWSGQTAICDNG 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24 GTGLYPMRGPFKNLALLPFSLPLIGGG-------GSGSGEKVSV-------60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 GSNLSP-----QLCLMPFILGLLSGGVTTTPWSLARPQGSCSLEGVEIKGGSFRLLOEG 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pimenta A.F., Fischer I., Levitt P., "cDNa cloning and structural analysis of the human limbic-system-associated membrane protein (LAMP).", Gene 170:189-195(1996).

-: FUNCTION. MEDIATES SELECTIVE NEURONAL GROWTH AND AXON TARGETING.
-: FUNCTION. MEDIATES SELECTIVE NEURONAL GROWTH AND AXON TARGETING.
-: THE HYPOCAMPAL MOSS FIBER PROJECTION (BY STMILLARITY).
-: SUBCELLULAR LOCATION: A KLACAGE to the membrane by a GPI-anchor.
-: TISSUE SPECIFICITY: EXPRESSED ON LIMBIC NEURONS AND FIBER TRACTS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 62; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AS WELL AS IN SINGLE LAYERS OF THE SUPERIOR COLLICULUS, SPINAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Eutuleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -: SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. IGLON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Limbic system-associated membrane protein precursor (LSAMP)
                                                                                                                                                                                                                                                                                                                                                                                                 Length 764;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 71; Indels
                                                                                                                                                                                                                                                                                                                                                                                                 5.8%; Score 83; DB 1;
24.1%; Pred. No. 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     338 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                 21; Mismatches
                         interpro; 1PR001254; Ser_protease_fry.interpro; IPR000436; Sushi_SCR_CCP.
Interpro; IPR002035; VWF_A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             157 VGFFK----PISCRNVNGYSYKV 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           162 AGYCSNPGIPIGTRKV-GSQYRL 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
InterPro; IPR001314; Chymotrypsin
                                                                                                                                                                                                                                                                                             PROSITE, PS50240; TRYPSIN_DOM; 1. PROSITE; PS00134; TRYPSIN_HIS; 1. PROSITE; PS00135; TRYPSIN_SER; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. MEDLINE-96235133; PubMed-8666243;
                                                                                                                                                                   PRINTS; PROO72; CHYMOTRYPSIN.
PRINTS; PRO0453; VWFADOMAIN.
SMART; SM00032; CCP; 3.
SMART; SM00020; TCP_SPC; 1.
SMART; SM000327; VWA: 1.
                                                                                                Pfam; PF00084; sushi; 3.
Pfam; PF00089; trypsin; 1.
Pfam; PF00092; vwa; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 49; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CHORD AND CEREBELLUM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human).
```

8

```
evolution.";
                                                                                                                                                                                                                                                            ENT1_HUMAN
                                                                                                                                                                                                                                                                      Cp
                                                                                                                                                                                                                        a
  8
     modified and this statement is not removed. Usage by and for communcial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                  101 SAGGEESLKCEDLKVG----OYICKDPKINDATQEPVNCTNYTAHVSCFPAPNITCKDSS 135
                                                                                                                                                                                                                                                                                                                                                                                                                               230 TIGROASLKCEASAVPAPDFEWYRDDTRINSANGLEIKSTE---GOSSLTVTNVT-FEHY 285
                                                                                                                                                                                                                                                                                                                                                                                                                     157 GNETHFTGNEVG-----FFKPISCRNVNGYSYKVAVALSLFLGWLGADRFYLGYPALG 209
  is in no
                                                                                                                                                                                                                                                                                                                                                                  27; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE=98300335; PubMed=9636706;
Ford M.E., Sarkis G.J., Belanger A.E., Hendrix R.W., Hatfull G.F.;
"Genome structure of mycobacteriophage D29: implications for phage
                                                                                                                                                                                                                                                          (POTENTIAL).
(POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae
NCBI_TaxID=28369;
                                                                                                                                                                                     REMOVED IN MATURE FORM (POTENTIAL), IG-LIKE C2-TYPE 1. IG-LIKE C2-TYPE 2. IG-LIKE C2-TYPE 3.
                                                                                                                                                                                                                                                                                    (POTENTIAL)
                                                                                                                                                                                                                                                                                                      (POTENTIAL)
                                                                                                                                                                                                                                                    (POTENTIAL)
                                                                                                                                          adhesion: Glycoprotein: GPI-anchor;
                                                                                                                                                           POTENTIAL,
LIMBIC SYSTEM-ASSOCIATED MEMBRANE
                                                                                                                                                                                                                                                                                                                                                5.7%; Score 82.5; DB 1; Length 336;
  as its content
                                                                                                                                                                                                                                                                                                                                                                 47; Indels
                                                                                                                                                                                                                                                                                                                                03455F286DF5D92F CRC64;
                                                                                                                                                                                                                                                 N-LINKED (GLCNAC...)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                        5.2;
                                                                                                                                                                                                                                                                                                                                                                14; Mismatches
institutions as long
                                                                                                                                                                                                                                                                                                                                                         Pred. No.
                                                                                                                                                                                                                        POTENTIAL
                                                                                                                                                                                                                                  POTENTIAL
                                                                                                                                                                                                                                         POTENTIAL
                                                                                                                                                                             PROTEIN.
                                                                     MIM; 603241; -.
GO; GO:0007399; P:neurogenesis; TAS.
                                                                                     InterPro: IPR007110; Ig-like.
InterPro: IPR003598: Ig_c2.
InterPro: IPR003006: Ig_MHC.
                                                                                                              Pfam; PF00047; ig; 3.
SMART; SM00408; IGC2; 2.
PROSITE; PS50835; IG_LIKE; 3.
Immunoglobulin domain; Cell a
                                                                                                                                                                                                                                                                                                                                37308 MW;
                                          EMBL; U41901; AAC50569.1; -. PIR; JC4776; JC4776.
                                                                                                                                                                                                                                                                                                                                                        29.68;
                                                                                                                                                                                                                                                                                                                                                                37; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                            Genew: HGNC:6705; LSAMP.
                                                                                                                                                           315
                                                                                                                                                                                     338
122
214
304
111
197
290
                                                                                                                                                                                                                                                 40
66
136
148
279
279
300
315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gene 32 protein (GP32)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mycobacteriophage D29
non-profit.
                                                                                                                                                                                                                                                                                                             315
315
338 AA;
                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                       210 LLKFC 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LLSKC 338
                                                                                                                                                                                                                                                                   136
148
279
287
300
                                                                                                                                                    Repeat; Signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VG32_BPMD2
O64226;
                                                                                                                                                                                                                                                                   CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                    CARBOHYD
CARBOHYD
                                                                                                                                                                                                               DOMAIN
DISULFID
                                                                                                                                                                                                                                                                                                              CARBOHYD
                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                DISULFID
                                                                                                                                                                                                                                         DISULFID
                                                                                                                                                                                                                                                  CARBOHYD
                                                                                                                                                                                                                                                           CARBOHYD
                                                                                                                                                                                                                                                                                                       CARBOHYD
                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                         Best Local
                                                                                                                                                           SIGNAL
                                                                                                                                                                                     PROPEP
DOMAIN
                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                                                       LIPID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VG32_BPMD2
                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 11
ò
                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                     93
                                                                                                                                                                                                                                                                                                                                                                                                                                                        ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        q
```

```
the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no wey modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                               This SWISS-PROT cntry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             37 PVLTPVTAVGAYTYNIPAQAEFIDVILLGAGGGGGG-----MGSAIAWGOGGFGGSWVTA 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE-Jejunum, and Small intestine;

"Critical Structural determinants for high affinity binding of
nucleosides to the equilibrative NBMPR sensitive nucleoside
transporter (es) cloned from the human jejunum.";
submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases
i-FUNCTION: MEDIATES BOTH INFLUX AND EFFLUX OF NUCLEOSIDES ACROSS
I-FUNCTION: MEDIATES BOTH INFLUX AND EFFLUX OF NUCLEOSIDES ACROSS
I-FUNCTION: MEDIATES BOTH INFLUX AND EFFLUX OF NUCLEOSIDES OF THE INHIBITOR NITROBENZYLMERCAPTOPURINE
RIBOSIDE (NBMPR) AND IS SODIUM: INHIBITED BY DIPYRIDAMOLE AND DILAZEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29 PMRGPFKNLALLPFSI.P-----LLGGGGSGGEKVSVSKMAAAWPSGPSAPEAVTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUR-Placenta;
MEDIATINE-971A0266; PubMed=8986748;
Griffitis M., Beaumont N., Yao S.Y.M., Sundaram M., Bouman C.E.,
Davies A., Kwong F.Y.P., Coe I., Cass C.E., Young J.D., Baldwin S.A.;
"Cloning of a human nucleoside transporter implicated in the cellular uptake of adenosine and chemotherapeutic drugs.";
Nat. Med. 3:89-93(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Equilbrative nucleoside transporter 1 (Equilibrative nucleoside transporter)
nitrobenzylmercaptopurine riboside sensitive nucleoside transporter)
(Equilibrative NBMPR-sensitive nucleoside transporter)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (ANTICANCER CHEMOTHERAPEUTICS DRUGS).
-!- SUBCFLLULAR LOCATION: Integral membrane protein.
-!- TISSUE SPECIFICITY: EXPRESSED IN HEART, BRAIN, MAMMARY GLAND,
ERYTHROCYTES AND PLACENTA, AND ALSO IN FETAL LIVER AND SPLEEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -! - SIMILARITY: BELONGS TO THE SLC29A FAMILY OF TRANSPORTERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 223;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AF022214; AAC18473.1; -.
PIR; F72803; F72803.
SEQUENCE 223 AA; 21822 MW; 33CD0DC310038AD4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                455 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ouery Match 5.6%; Score 80.5; DI Best Local Similarity 30.7%; Pred. No. 4.8; Matches 27; Conservative 8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 92 TLRRGVDIPWAVTQITGVIGAGGTAGPG 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         80 RL---VGVLWFVSVTTGPWGAVATSAGG 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A., AND SEQUENCE OF 1-21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
J. Mol. Biol. 279:143-164(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       transporter, es-type).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PTM: GLYCOSYLATED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ENTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ENT 1_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SLC29A1 OR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                808560
```

328 AA

STANDARD;

σ

```
LBP2_HUMAN
    This SWISS-PROI entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBS outstation the European Bioinformatics Institute. There are no restrictions on its way non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                128 AIQEPUN--------CTNYTAHVSGFPAPNITCKDS-SGNEIHFTGNEV 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            156 LQGSLFGLAGLLPASYTAPIMSGQGL-AGFFASVA-MICAIASGSELSESAFGYFITACA 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             82 VGVLWFVSVTTGP-----WGAVATSAGGEESLKCEDLKVGQYICKDPK------1NC 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30 MRGPFKNLA-LLP--FSLPLLGGGGSGSGEKVSVSKMAAAWPSGPSAPEA----VTARL 81
                                                                                                                                           TAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-LINKED (GiCNAC. . .) (POTENTIAL). 9098E95E26515850 CRC64;
                                                                                                       ; 602153; -. Goods and the control of plasma membrane: TAS. GO:0005804; C:integral to plasma membrane: TAS. GO:0005817; F:nucleoside transporter activity; TAS. GO:0005337; F:nucleoside transporter activity; TAS. GO:0006139; F:nucleoside transporter activity; TAS. GO:0015858; P:nucleoside transport; TAS. GO:0015859; DER/eqnu_transport.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     168 GFFKPISC-RNVNGYSYKVAVALSLFLGWLGADRFYLGYPALGLLKFCTV 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               325 RYFIPVSCFLTFNIFDWLGRSLTAVFM-WPGKDSRWL--PSLVLARLVFV 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1; Length 455;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       82; Indels
                                                                                                                                                                                                                                                                                                                                                         EXTRACELLULAR (POTENTIAL).
POTENTIAL.
                                                                                                                                                                                                                                                                        POTENTIAL.
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                    EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                              EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL.
EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                 EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL. CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                     POTENTIAL.
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                       CYTOPLASMIC (PCTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                           CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                  CYTOPLASMIC (POIENTIAL).
                                                                                                                                                                                                                          CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                            5.6%; Score 80.5; E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     39; Mismatches
                                                                                                                                                                                                                                                                                                             POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No.
                                                                                                                                                                  Pfam: PF01733; Nucleoside_tran; 1.
PRIMTS; PR01130; DERBYTRNSFRT.
ProDom; PD005103; DER/eqnu_transpt; 1.
TIGRPAMS; TIGR00939; 2a57; 1.
                                                                                                                                                                                                         Transport; Glycoprotein.
                                                                                                                                                                                                                                                                                                                               POTENTIAL
                                                                                                                                                                                                                                                                                                                                                 POTENTIAL
                                                                                                                                                                                                                                                                                          POTENTIAL
                                                                                   AAC62495.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   50088 MW;
                                                                           EMBL; U81375; AAC51103.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ilarity 22.6%;
Conservative 3
                                                                                            HGNC:11003; SLC29Al.
                                                                                                                                                                                                                          11
28
81
81
106
1129
1137
1173
1198
1205
226
226
310
                                                                                                                                                                                                                                                                                                                                                        322
322
3321
3321
4412
4510
4510
                                                                                                                                                                                                                                                                                                                                                                                                                                452
47
455 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
es 52; Conserv
                                                                                                                                                                                                       Transmembrane; T
INIT_MET C
DOMAIN :
TRANSMEM 12
                                                                                                                                                                                                                                   12
29
82
107
                                                                                                      602193
                                                                                                                                                            InterPro;
                                                                                                                                                                                                                                                    TRANSMEM
DOMAIN
                                                                                                                                                                                                                                                                                                                    DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                             FRANSMEM
                                                                                                                                                                                                                                                                                                                                               IRANSMEM
                                                                                                                                                                                                                                                                                                                                                                  RANSMEM
                                                                                                                                                                                                                                                                                                                                                                                    FRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                       TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                         TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                           CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ouery Match
                                                                                                                                                                                                                                                                        TRANSMEM
                                                                                                                                                                                                                                                                                          LRANSMEM
                                                                                             Genew;
                                                                                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                                                                                                   DOMA1N
                                                                                                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Loca
Matches
                                                                                                                       00000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
  qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     οχ
```

RESULT 13 IBP2_HUMAN

```
TISSUE-Brain, and Uterus;

X MEDLINE-22388257; Pubmed-12477932;

A Klausner R.D., Feingold E.A., Grouse L.H., Derge J.G.,

Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

A Brownstein M.J., Usdin T.B., Toshlyuki S., Carninci P., Prange C.,

A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

A Rosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

A Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IISSUE-Fetal liver:
MEDLINE-90060007; PubMed-2479552;
Binkert C., Landwehr J., Mary J.L., Schwander J., Heinrich G.;
"Cloning, sequence analysis and expression of a cDNA encoding a novel insulin-like growth factor binding protein (IGFBP-2).":
EMBO J. 8:2497-2502(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A., AND SEQUENCE OF 40-77.

APDLINE-90368661: PubMed-1697583;

Zapi G., Kieler M., Merryweather J., Masiarz F., Bauer D., Born W.,

Fischer J.A., Foresch E.R.

"Isolation from adult human serum of four insulin-like growth factor (IGF) binding proteins and molecular cloning of one of them that is increased by IGF I administration and in extrapancreatic tumor hypoglycemia.".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE-Placenta;
MEDLINE-91248211; PubMed=17100112;
Ehrenborg E. Vilhelmsdotter S., Bajalica S., Larsson C., Sterm L.,
Ehrenborg E., Vilhelmson K., Luthman H.;
Koch J., Brondum-Nielsen K., Luthman H.;
"Structure and localization of the human insulin-like growth factor-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Binkert C., Margot J.B., Landwehr J., Heinrich G., Schwander J.; "Structure of the human insulin-like growth factor binding protein-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Aqarwal N., Hsieh C.L., Sills D., Swaroop M., Desai B., Francke U.
                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia; Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Sequence analysis, expression and chromosomal localization of a gene, isolated from a subtracted human retina cDNA library, that encodes an insulin-like growth factor binding protein (IGFBP2)."; Fxp. Eye Res. 52:549-561(1991).
                                                                                                                                                                                        precursor (IGFBP-2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 binding protein 2 gene.";
Biochem. Biophys. Res. Commun. 176:1250-1255(1991).
P18055; 014619;
01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Insulin-like growth factor binding protein 2 f
IGFPP2 OR BP2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Biol. Chem. 265:14892-14898(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE-Retina;
MEDLINE-91293227; PubMed-1712312;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE-Placenta:
MEDLINE-92293159; PubMed-1376411;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mol. Endocrinol. 6:826-836(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  [6]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Swarcop A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  dene.
```

94

```
-----AVAAVAGGAR-MPCAEL----VREPGCGCCSVCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Benkouka F., Guidoni A.A., de Caro J.D., Bonicel J.J., Descuelle P.A., Rovery M.;
                                                                                                                                                                                                                                                            450 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complex.";
J. Biol. Chem. 271:18007-18016(1996).
                                                                    129 TOEPVNCTNYTAH ---- VSCFPAP 148
                                                                                                                     95 RLEGEACGVYTPRCGOGLRCYPHP 118
                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eur. J. Biochem. 128:331-341(1982)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eur. J. Biochem. 97:395-405(1979)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=83105095; PubMed~7151781;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-82000578; Pubmed-6791692;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDI,INE=82113655; PubMed=7326260;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 235-307.
MEDLINE-80088446; PubMed=518929;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Biochimie 61:841-845(1979)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIRUCTURE OF CARBOHYDRATE.
                                                                                                                                                                                                                                                               STANDARD;
              62 APPA----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBSTRATE-BINDING SITE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 308-449.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the peptide chair.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sus scrofa (Pig).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DISULFIDE BONDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               amino acids
                                                                                                                                                                                                                                                               LIPP_PIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   droups.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         PNLIP
                                                                                                                                                                                                                                                                 REFERENCE AND THE SERVICE FRANKERS AND THE SER
                                                                    8
                                                                                                                     a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL CURSTALLON: the European Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an canal to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                œ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   73 APEAVTARLVGVLWFVSVTTGPWGAVATSAGGEESLKCEDLKVGQYICKDPKIN----DA 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22 RDGTGLYPMRGPFKNLALLPFSLPLLGGGGSGGKVSV-----SKMAAAWPSGPS 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Whiting M., Madan A., Young A.C., Shavchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska D., Saailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length Proc. Natl. Acad. Sci. U.S.A., 99:16899-16903(2002).

-!-FUNCTION: IGF-BIADING PROTEINS PROLONG THE HALF-LIFE OF THE JOYN AND HAVE BEEN SHOWN TO FITHER INHIBIT OR STIMULATE THE GROWTH PROMOTING EFFECTS OF THE GROSS ON CELE CULTURE. THEY ALTER THE INTERMINANT OF IGES ON THE LIBER CELL SURFACE RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INSULIN-LIKE GROWTH FACTOR BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  46:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ::
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5.6%; Score 60; DB 1; Length 328; 27.8%; Pred. No. 8.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                48; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               THYROGLOBULIN TYPE I.
CELL ATTACHMENI SITE.
P -> R (IN REF. 4).
R -> C (IN REF. 3).
H -> D (IN REF. 4).
A: 4E6BDF6D805C8853 CRC64;
                                                                                                                                                                                                                                                                                                                                         SUBCELLULAR LOCATION: Secreted.
MISCELLANEOUS: BINDS IGF-II MORE THAN IGF-I.
SIMILARITY: Contains 1 IGFBP domain.
SIMILARITY: Contains 1 thyroglobulin type-I domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MIM: 146731; -. CO. GO:0005209; F:plasma protein: TAS. GO: GO:0005209; F:plasma protein: TAS. InterPro: 1PR000867; Insl_gro_fac_pr. InterPro: 1PR000716; T:yroqlobulin_1. Pfam: PF00086; Thyroqlobulin_1: 1. SMART: SMG0221; IB: 1. SMART: SMO0211; TY: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROTEIN 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00222; IGE_BINDING; 1.
PROSITE; PS00484; THYROGLOBULIN_1; 1.
Growth factor binding; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  =
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               M69241, AAA36048.1;
M69237, AAA36048.1;
M69239, AAA36048.1;
M69239, AAA36048.1; JOINED.
M69240, AAA36048.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           $37712; AAB22308.1; JOINED.
$37722; AAB22308.1; JOINED.
$37726; AAB22308.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; A09809; CAA00862.1;
EMBL; BC004312; AA404312.1;
EMBL; BC009902; AA409902.1;
EMBL; BC012769; AA412769.1;
PIR; A41927; A41927
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               309
306
60
320
323
35137 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; S37730; AAB22308.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           M35410; AAA03246.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genew; HGNC:5471; IGFBP2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    39
328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 40; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            320
323
328 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1BOE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HSSP; P24593;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CONFLICT
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL;
EMBL;
EMBL;
EMBL;
EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL;
```

g

```
οĘ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Porcine pancreatic lipase. The disulfide bridges and the sulfhydryl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Guidoni A.A., Benkouka F., de Caro J.D., Rovery M.; Culdoni A.A., Benkouka F., de Caro J.D., Rovery M.; Characterization of the serine reacting with diethyl p-nitrophenyl phosphate in porcine pancreatic lipase. "; Biochim. Biophys. Acta 660:148-150(1981).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Lipase activation by nonionic detergents. The crystal structure of
the porcine lipase-colipase-tetraethylene glycol monooctyl ether
2: JUL-1986 (Rel. 01, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Triacylglycerol lipase, pancreatic (EC 3.1.1.3) (Pancreatic lipase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Porcine pancreatic lipase, Completion of the primary structure."; Biochim. Biophys. Acta 671:129-138(1981).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 1-234, AND CARBOHYDRATE-LINKAGE SITE.
MEDLINE-79236335; PubMed-380992;
Bianchetta J.D., Bidaud J., Giddoni A.A., Bonicel J.J., Rovery M.:
"Porcine pancreatic lipase. Sequence of the first 234 amino acids of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    de Caro J.D., Boudouard M., Bonicel J.J., Guidoni A.A., Desnuello Rovery M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDILINE-88062841; PubMed-3691527;
Fournet B., Leroy Y., Montreuil J., Decaro J., Rovery M.,
Van Kuik J.A., Vilegenthart J.F.G.;
"Primary structure of the glycans of porcine pancreatic lipase.";
Eur. J. Blochem. 170:369-371(1987).
                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Guidoni A.A., Bonicel J.J., Bianchetta J.D., Rovery M.;
"Porcine pancreatic lipase. Sequence between the 235th and 307th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS), AND REVISIONS TO 30-32. MEDLINE-56279347; Pubmed-8663362; Hermisco J., Pignol D., Kerfelec B., Crenon I., Chapus C., Fontecilla-Camps J.C.;
```

us-09-852-100a-2.rsp

```
DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CARBOHYD
CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TRANSMEM
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMAIN
      SONT THE PERMENT OF THE STANKING WAS A STANKING OF THE PERMENT OF THE STANKING OF THE STANKING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .
?
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                G
G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        85 LWFVSVTTGPWGAVAISAGGEESLKCEDLKVGQYICKDPKINDATGEPVNCINYTAHVS· 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MHILKGSPNVIP-----RAHGQKNIRRDG-----TGLYPMRGPFKNLALL--- 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              <del>7</del>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gerhardt C.C., Bakker R.A., Piek G.J., Planta R.J., Vreugdenhil E.,
Leysen J.E., van Heerikhuizen H.;
"Molecular cloning and pharmacological characterization of a molluscan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      193 DPSDAKFVDV1HTDAAPIIPNLGFGMSQTVGHLOF---FPNGGKOMPGCOKNILSQIVDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        133 VEVLKSSLGYSPSNVHVIGHSLGSHAAGEAGRRTNGTIERITGLDPAEPCF@GTPELVRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----PFSLPLLGGGGSGSKWSVSKMAAAWPSG----PSAPEAVTARLVGV
                                                          -i- SIMILARITY: BELONGS TO THE ABHYDROLASE SUPERFAMILY. LIPASE FAMILY:
-i- SIMILARITY: Contains 1 PLAT domain.
-i- DATABASE: NAME-Worthington enzyme manual;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            250 -----DGIW-----EGTRDFVACNHIRSYKYYA-SSILNPDGFAGFPCDSYNVFTAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Saps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lymnaea stagnalis (Great pond snail).
Eukaryota: Metazoa: Mollusca: Gastropoda: Pulmonata; Basommatophora;
Lymnaeoidea; Lymnaeidae: Lymnaea.
NCBI_TaxID=6523;
                                                                                                                                                                                                                                                                                                                              Lipid degradation: Pancreas; Glycoprotein: 3D-structure. 339 450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        296 KCFPCPSEGCPQMGHYADRFPGKTNGVSQVFYLNTGDASNFARWRYKVSVTLS 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  144 - CFPAPNITCKDSSGNETHFTG-----NEVGFFKPISCKNVNGYSYKVAVALS 190
CAIALYTIC ACTIVITY: Triacylglycerol + H(2)0 = diacylglycerol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            :09
                                                                                                                  WWW-*http://www.worthington-biochem.com/manuai/L/P5.html",
PDB; 1ETH: 07-DEC-96.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5.6%; Score 80; DB 1; Length 450; 20.2%; Pred. No. 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            96; Indeis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-LINKED (GLCNAC. ..).
76E13BBDB4541E0E CRC54;
                                                                                                                                                                                                                                                                                                                                                                    CHARGE RELAY SYSTEM CHARGE RFLAY SYSTEM
                                                                                                                                                                                                                                                                                                                                                                                                            CHARGE RELAY SYSTEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Octopamine receptor 1 (OA1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      638 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                              IN ISOMER 1.
IN ISOMER 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A., AND CHARACTERIZATION.
                                                                                                                                                  InterPro: IPRC00734; Lipase.
InterPro: IPRC01024; Lipoxygenase LH2.
InterPro: IPRC01034; Lipoxygenase LH2.
InterPro: IPRC01037; Ser_estrs_site.
Pfam: PFC0151; lipase: 1.
Pfam: PFC0177; PLAY: 1.
PRINTS: PRC0821: TAGLIPASE.
                                        -!- SUBCÉLLULAR LOCATION: Secreted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-97347296; Pubmed=9203635;
                                                                                                                                                                                                                                                                                        PROSITE; PS00120; LIPASE_SER; 1.
PROSITE; PS50095; PLAT; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  50084 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                            10
102
104
262
297
305
450
                                                                                                                                                                                                                                                                                                                                                                    153
177
264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    octopamine receptor."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Thes 47; Conservat
                        fatty acid anion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              167
450 AA;
                                                                                                                                                                                                                                                                                                                                                                      153
                                                                                                                                                                                                                                                                                                                                                                                                          264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OAR1_LYMST
077408;
                                                                                                                                                                                                                                                                                                                              Hydrolase;
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IISSUE-CNS
                                                                                                                                                                                                                                                                                                                                                                                    ACT_SITE
ACT_SITE
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                DISOLFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DISULFID
                                                                                                                                                                                                                                                                                                                                                                    ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 15
  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ô
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (Soc http://www.isb-sib.ch/announce/or send am email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ··
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         149 NITCKD-----SSGNETHFTGNEVGFFKPISCRNVNGYSYKVAVALSLFLGWLGA 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 199 DRFY-----LGYPALGLLKFCTVGFCGIGSLIDFILISMQIVGPSDGSSYIIDYYGTRLT 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        69 NLACADLLLGVLVLPFSAVNEI----KDVWIFGHVWCOVWLAVDVWI.CTASII.NI.CCISI. 124
MOL: Pharmacol. 51:293-300(1997).
-!- FUNCTION: G-PROTEIN COUPLED RECEPTOR FOR OCTOPAMINE (OA), WHICH 1S
                                                                                    A NEUROTRANSHITTER, NEUROHORMONE, AND NEOROMODULATOR IN INVERTEBRATES. ACTIVATION OF THIS RECEPTOR BY OCTOPAMINE INDUCES OF ALL INDUCES AND INCREASE IN BOTH INOSITOL PHOSPHATES AND CYCLIC AMP. THE COUPLING TO ADENIZI CYCLES SEEMS TO BE LESS EFFICIENT THAN THE COUPLING TO PHOSPHOLIPASE C. THE RANK ORDER OF POTEMOY FOR AGONISTS IS P-SYNEPHRINE >= CLONDINE > P-OCTOPAMINE = PHYPROMINE >= PHENYLEPHRINE > NOREPINEPHRINE > B-HT920 > SEROIONIN = P-TYRAMINE > EPINEPHRINE > NOREPINEPHRINE > METHOXAMINE > DOPPAXINE = HISTHAINE | SEPINEPHRINE > HENTOLARIA | SEROIONIN > P-TYRAMINE > HORDOMAZINE | SPINEPHRINE > PHENTOLAMINE > P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- SUBSCELLULAR LOCATION: Integral membrane protein.
-!- TISSUE SPECIFICITY: EXPRESSED IN THE CENTRAL NERVOUS SYSTEM.
-!- SIMILARITY: BELCNGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPIORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MIANSERINE > RAUWOLSCINE > PRAZOSIN > ALPRENOLOL / PROPANOLOL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BY SIMILARITY.

N-INKED (GLCNAC. ..) (POTENTIAL).

N-INKED (GLCNAC. ..) (POTENTIAL).

(ACTUAL)

(ACTUAL)

(ACTUAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1; Length 638;
18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          56; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HSSP; P29274; IMMH.
InterPro: IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm_1: 1.
PRINTS, PR00237; GPCRHODDPSN.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
G-protein coupled receptor; Transmembrane: Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EXTRACELLULAR (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-LINKED (GLCNAC. . .) (P
65FA928B5C01D34F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .8%; Pred. No. ...
e 18; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5.6%; Score 80;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  70000 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; U62771; AAC61296.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 24.8
Matches 31; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       521
546
552
576
178
207
215
638 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               254 RISIT 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        184 PIPVT 188
```

Search completed: September 26, 2003, 17:25:45

Job time : 26 secs

New peptide vector Signal sequence ba Signal sequence ba Signal sequence ba Signal sequence ba Drosophila melanoq Human beta amyloid Human secreted pro Human secreted pro DNA encoding a mur A human TANGO 223 Drosophila melanog

AAU78348 ABG75506 ABB82542 ABB65236 Human ORF40. Homo Human PRO1489 (UNC Protein of the inv Novel human diagno pr53.3 (NCIMB 4030

Human polypeptide Human ORF40. Hom

AAY70761 ABR47818 ABR47818 ABR01112 AAY2758 AAB08641 AAB08656 AAB08657 AAB08658 ABB59014 AAB08658 ABB59014 AAB08658 ABB59014 AAB08658 ABB59014 AAB08658 ABB59014 AAB08658 ABB59014 AAB08658 AAB0868 AAB0868

GenCore version 5.1.5 Copyright (c) 1993 - 2003 Compugen Ltd.

using sw model protein search, OM protein

Run on:

September 26, 2003, 17:28:58; search time 16.7106 Seconds (without alignments) 313.452 Million cell updates/sec

US-09-852-100A-2_COPY_185_217 Title: Perfect score:

1 VAVALSEFIGWLGADRFYLGYPALGLIKFCTVG 33 OLIGO Gapop 60.0 , Gapext 60.0 Scoring table: Sequence:

1107863 seqs, 158726573 residues Searched:

0

Word size :

1107863 Total number of hits satisfying chosen parameters:

length: 0 length: 2000000000 Minimum DB seq Maximum DB seq

Post-processing: Listing first 45 summaries

Database :

CONTRACTOR OF COLUMN	Human claudin-D17	Human secreted pro	Streptococcus poly	Human ORFX ORF2314	Human carbamoyl pł	Human protein segu	Human mitochondria	Aspergillus fumiga	Aspergillus fumiga	Human secreted pro	Propionibacterium.	T cell epitope/MHC	MHC class 1 molecu	Peptide identified	
	AAE22228	AAB39030	ABP26809	AAB42550	AAY44453	AAB92615	AAE33210	ABJ25413	ABJ26013	ABJ10922	AAU56553	AAY10404	ABG80086	AAB08587	
1	23	21	23	21	21	22	24	24	24	23	22	20	23	21	
1	224	367	466	469	469	469	695	785	864	869	1240	Q,	Q,	i	
	21.2	21.2	21.2	21.2	21.2	21.2	21.2	21.2	21.2	21.2	21.2	18.2	18.2	18.2	
	7	۲-	7	7	7	7	۲-	7	7	7	7	9	9	9	
	3.2	33	34	35	36	3.7	38	39	07	.T	42	43	75	45	
_															-

ALIGNMENTS

BAP;

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being prin and is derived by analysis of the total score distribution.

Human beta-a Human BBP-1 Human 5' ES1 Human secret Signal segue Cell penetra Fluorescentl Humar beta-New peptide Description SUMMARIES AAW94291 AAY70759 AAE33877 AAY12358 ABY12358 ABB11574 ABB11568 ABB778990 AAE23685 Π 23 23 23 23 23 23 23 23 23 DB Length 269 269 269 139 225 225 24 27 27 Query Match 100.0 100.0 100.0 27.3 24.2 24.2 24.2 Score 01 M 4 M 90 F 80 M Result Š.

21.2 469 24 AAE33210	7 21.2	7 21 2 864 24 ABT26013	7 7 864 73 ABITO922	7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7	ACACCAC CC C	10101010101010101010101010101010101010	3 23 ABGBUURO	77 17 7:01 0		ALIGNÆNTS			REGULT 1	AAW94291	AAW94291 standard: Protein: 269 AA.		AAW94291;		27-APR-1999 (first entry)		Human beta-amyloid peptide-binding protein (BBP).		Beta-amyloid peptide binding protein; BBP; beta-amyloid protein;	human; Alzheimer's disease.		Homo sapiens.	Kev Location/Onalifiers	ion		beta-amyloid peptide binding activity"		WO9846636-A2.		22-0CT-1998.		14-APR-1998; 98WO-US07462.		16-APR-1997; 97US-0064583.		(AMHP) AMERICAN HOME PROD CORP.		Bard JA, Jacobsen JS, Kajkowski EM, Ozenberger BA:	Walker SG;
													RESU	AAW9	G	××	AC.	××	LT	××	30	XX	χ Σ.	X	XX	s ×	H	FT	FI	FT	××	N.	×	PD	××	۳. ت	XX	e.d.	××	ΡĄ	×	PI	PI
		-emp1/AA1980.DAT:*	/AR1981	- PED) /AA '980 DAT *			- CHILL / ARIYON - DAI :			-embi/AA1988.DAT:*	/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1989.DAT:•	p-embl/AA1990.DAT:*	/SIDS1/gcgdata/geneseq/geneseqp-ombi/AA1991.DAT:*	/SIDS1/gcgdata/geneseq/genesegp-embi/AA1992.DAT:*	/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1993.DAT:•	/SIDS1/gcgdata/geneseq/qeneseqp-emb1/AA1994.DAT:*	'SIDS1/gcgdata/geneseg/genesegp-emb1/AA1995.DAT:*	'SIDS1/gcgdata/geneseq/qeneseqp-emb1/AA1996.DAT:*	SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1997.DAT:	SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1998.DAT:*	/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1999.DA1:*	SIDS1/gcgdata/gcneseq/geneseqp-embl/AA2000.DAT:*	SIDSI/gcgdata/geneseq/geneseqp-emb1/AA2301.DAT:*	SIDS1/gcgdata/geneseq/geneseqp-embl/AA2002.DAT:*	sinsi/yoguara/yeneseg/yenesegp-embi/AAzoos.bAi:*	by chance to have a	greater than or equal to the score of the result being printed.	derived by analysis of the total score distribution.					Description		Human beta-amyloid	Human beta-anyloid	Human BBP-1 protei	Human 5' ESl secre	Human secreted pro	New peptide vector	Signal sequence ba	Cell penetrating p	Fluorescently labe
		/SIDS1/accdata/geneseg/genesegp-embl	/SIDS1/goddata/geneseg/genesegp-embl	SIDSI/acadata/geneseg/genesegp-eghl	(SIDSI/acadata/aeneseo/aenesean-embl	Cincil / dedented / demended / demended from the control of the co	Sinsily goddard, genesedy genesedpremer (SIDS) (goddard (genesed) genesedpremer	SIDSI/yedata/yenesed/yenesedp_empI	SIDSI/gcgdata/geneseq/geneseqp-embl	SIDS1/gcgdata/geneseq/geneseqp-embi	ed/acnesed:	/SIDS1/gcgdata/geneseg/genesegp-emb	ibasaua5/bas	sed/denesed	sed/denesed	sed/denesed	sed/denesed	sed/denesed	besed/denesed	lbasaua6/basa	bəsəuə6/bəsə	esed/denesed	ibəsəuəb/bəsə	lbəsəuəb/bəsa	Sed/denesed!	No. is the number of results predicted by c	score of the	total score		SUMMARIES					AAW94291	AAY70759	AAE33877	AAY12358	ABB11574	ABB77688	ABB81176	ABG78990	AAE23685

```
N-PSDB; AAZ52369.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAE33877
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ें
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ΩÞ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                The present sequence represents a beta-amyloid peptide binding pratein (BBP). The polynuclocide comprising the entire BBP nucleotide sequence of clone BBP1-f1 is deposited under the accession number ATCC 96617. The polynucleotide comprising a fragment of BBP (nucleotides 202-807 of the full length BBP) of clone pEK196 is deposited as ATCC 98399. Host cells transformed with a vector comprising the BBP nucleic acid are used for the recombinant production of the protein. The protein can be used in a method for diagnosing a disease characterised by aberrant expression of human beta-amyloid protein (BAP). The protein can also be used in a method for screening for compounds which regulate expression of a 3AF binding protein. The proteins, antibodies and identified compounds can be used in the treatment or prevention of Alzheimer's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            199..201
/Jabel- DRF_motif
/note- "Substitution of the Arg abrogates protection"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Beta-amyloid peptide binding protein, BBP, BAP, tumour, supprossor, G-protein coupled receptor; GPCR, integral membrane protein; antiquen neuronal cell; nonhuman primate; MBP; G-protein signalling pathway; apoptosis; immunogen; therapeutic, treatment; prevention; diagnosito.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                       Polynucleotide encoding beta-amyloid peptide binding protein - used to identify inhibitors of beta-amyloid peptide for treating Alzheimer's disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 269;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human beta-amyloid peptide (BAP) binding protein, BBP1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 33; DB 20; 100.0%; Pred. No. 3.9e-24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 185 VAVALSLFLGKLGADRFYLGYPALGLLKFCTVG 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /label Transmembrane_domain_2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     177..198
/iabcl- Transmembrane_domain_1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 VAVALSLFLGWLGADRFYLGYPALGLLKFCTVG 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kajkowski EM, Lo CF;
                                                                                                                                                                           Claim 7; Pages 43-44; 59pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Socation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY70759 standard; Protein; 269 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (AMHP ) AMERICAN HOME PROD CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98US-0104104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99WO-US21621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24-JUL-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             33; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               213..238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2000-317982/27
                      WPI: 1999-080736/57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match
Best Local Similarity
Matches 33; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          269 AA;
                                           N-PSDB; AAX05735
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ozenberger BA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200022125-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Home sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20-APR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY70759;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY70759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       X X X DD X X B DD X B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    qq
```

```
ó
                                                                                                                                                                                                  The present sequence is the beta-amyloid peptide (BAP) binding protein-1 (BBP1). It is an integral membrane protein, that traverse the membrane twice. It is related to 6 protein-coupled receptor (GPCA) protein supertamily. It interacts with 6-alpha proteins and regulates the activity of G-protein signalling pathways. BBP genes are widely expressed in newronal cells of nonhuman primate (NHP) brain and overexpressed in some tumours. It functions as a suppressor of apoptosis induction. BBP proteins are used as immunogens to raise antibodies, useful as proteins are against so lidentify molecules which effect the interaction of BBP as reagents to identify molecules which effect the interaction of BBP and a cloned protein, that are useful in the treatment or prevention of diseases associated with apoptosis. The polynucleotides are useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Noté: In claim 5, the patent claims an amino acid sequence from figure However, figure 2 does not contain any sequence. It is inferred from the disciosure that the figure 2 sequence refers to BBPI protein, shown in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; beta-amyloid peptide-binding protein; BAP; Abeta; betaAP; BBP; Alzheimer's disease; AD; transgenic; transgenic animal; gene therapy; neuroprotective; nootropic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New human beta-amyloid peptide-binding protein, useful for diagnosing and/or treating diseases associated with aberrant expression of beta-amyloid peptide, e.g. Alzhelmer's disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
Novel 3-protein-coupled receptor-like proteins and polynucleotides useful for regulating apoptosis, comprises integral membrane protein traversing the membrane twice.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Walker SG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 269;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        JA, Kajkowski EM, Jacobsen JS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 33; DB 21; 100.0%; Pred. No. 3.9e-24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         185 VAVALSLFLGWLGADRFYLGYPALGLLKFCTVG 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 VAVALSLFLGWLGADRFYLGYPALGLLKFCTVG 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                            Example 1; Page 62-63; 68pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAE33877 standard; Protein; 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ċ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       06-MAY-2002; 2002WO-US14223.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               09-MAY-2001; 2001US-0852100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ozenberger BA, Bard J
Sofia HJ, Howland DS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human BBP-1 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2003-120537/11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
Matches 33; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        269 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; AAD51940.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     W0200290499-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (AMHP ) WYETH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Home saptens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C2-MAY-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     diagnostics.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14-NCV-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sednence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAE33877;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 3
```

```
٥
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         human secreted proteins, and encode the proteins given in ANT12261 to AANT22161 to and an N-terminal fragment of a secreted protein. The nucleic acid sequences can be used for producing secreted human gene products. They can also be used to develop products for diagnosis and therapy. The proteins obtained may have cytokine activity, cell proliferation/differentiation activity, haematopoiesis regulating activity, tissue growth regulating activity, haematopoiesis regulating activity, receptor/ ligand activity, activity, haemosciatic and thrombolytic activity, receptor/ ligand activity, activity, activity activity, activity, the activity activity, activity activity, activity activity, activity activity activity, activity activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   forensic; gene therapy; chromosome mapping; signal peptide; upstream regulatory sequence; cytokine activity; cell proliferation; differentiation; haematopolesis regulation; tissue growth regulation; reproductive hormone regulation; chemotactic; chemokinetic; haemostatic; thrombolytic; anti-inflammatory; tumour inhibition.
                                                                                                               The present invention relates to novel human beta-amyloid peptide (BAP). Abeta, betaAP)-binding (BBP) proteins and polynucleotides encoding such proteins. BBP sequences are useful to diagnose and/or treat diseases associated with aberrant expression of human BAP such as Aizheimer's disease (AD). They are used to generate transgenic animals. Sequences of the invention are also used in gene therapy. The present sequence is human BBP-1 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAX41094 to AAX41347 represent 5' expressed sequence tags (ESTs) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New nucleic acids encoding human secreted proteins - obtained from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cDNA libraries prepared from e.g. liver, ovary, brain, prostate, kidney, lung, umbilical cord, placenta and colon tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; secreted protein; EST; expressed sequence tag; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 269;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 33; DB 24; 100.0%; Pred. No. 3.9e-24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               185 VAVALSEFLGWEGADRFYLGYPALGELKFCTVG 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lacroix B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 VAVALSLFLGWLGADRFYLGYPALGLLKFCTVG 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human 5' EST secreted protein SEQ ID NO:389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 27; Page 714-715; 824pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Duclert A, Dumas Milne Edwards J,
Claim 4; Page 84-85; 85pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY12358 standard; Protein; 139 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98WO-IB01222.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    33; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI: 1999-153778/13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              269 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; AAX41191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (GEST ) GENSET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           W09906548-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11-FEB-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY12358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     \mathcal{S} \times \mathcal{S} \cup \mathcal{S} \cup
```

```
.
O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and sequences ABA08225-ABA09574 represent nucleic acids encoding them. The invention also relates to vectors and recombinant host cells comprising nuclectide of the invention, methods of producing the novel polypeptides, antibodies against the polypeptides, methods of detecting the nuclectides or polypeptides in a sample, and methods of identifying compounds which bind to polypeptides of the invention. Although novel, many of the polypeptides of the invention have homology to known proteins, thereby
can be used in forensic, gene therapy and chromosome mapping procedures. The sequences can also be used for obtaining corresponding promoter sequences. The nucleic acids encoding the signal peptide can be used for directing extracellular secretion of a polypeptide or the insertion of a polypeptide into a membrane, or importing a polypeptide into a cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; cytokine; cell proliferation; cell differentiation; growth factor haematopoiesis regulation; tissue growth; immunomodulator; activin; inhibin; chemotaxis; chemokinesis; thrombolysis; oncogenesis; proliferation; metastesis; cancer; tumour; haematopoietic disorder; myeloid cell disorder; lymphoid cell disorder; propietic disorder; chronic inflammatory condition; proliferative retinopath; chronic inflammatory condition; proliferative retinopath; bone disorder; osteoporosis; vascular growth disorder; cell culture; drug screening; infection; immune disorder; artissue regeneration; wound healing; infection; immune disorder; antisture; drug screening; gene therappy; antisifialammatory; antisthritic; haemostatic; antisateriosclerotic; cytostatic; osteopathic; vascupolic; cardiant; virucide; antibacteriai; antifungal; vulnerary; antiulcer.
                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human proteins and DNA encoding sequences useful for preventing, treating or ameliorating a medical condition in a mammalian subject
                                                                                                                                                                                                                        .:
                                                                                                                                                                               Length 139;
                                                                                                                                                                                                                      0; Indeis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human secreted protein homologue, SEQ ID NO:1944.
                                                                                                                                                                             51.5%; Score 17; DB 20; 1
100.0%; Pred. No. 6.9e-09;
                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 20; Page 214; 1963pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                        ABB11574 standard; peptide; 225 AA.
                                                                                                                                                                                               100.0%; Pr
                                                                                                                                                                                                                                                                                                              123 VAVALSLFLGWLGADRF 139
                                                                                                                                                                                                                                                                   1 VAVALSLFLGWLGADRF 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tang YT, Liu C, Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     05-FEB-2001; 2001WO-US0380G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         03-FEB-2000; 2000US-C495914
27-APR-2000; 2000US-C560875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        e.g. arthritis and cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                      Best Local Similarity 100.
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-457740/49.
                                                                                                                                       139 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; ABA08818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               W0200157188-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          09-AUG-2001
                                                                                                                                         Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABB11574;
                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          82888888
                                                                                                                                                                                                                                                                       á
```

length

```
The invention relates to a transfection agent comprises a peptide of about 16 - 30 amino acids in length. Peptides of the invention comprise a hydrophobic domain, a hydrophilic domain, a poptionally a spacer sequence between the domains and a functional group conjugated to at least one terminal of the peptide. Peptides of the invention are useful for a non-covalent association with and transport of a heterologous compound into a cell. They are also useful for promoting the cellular into a cell. They are also useful for promoting the cellular internalisation of at least one member e.g. peptide, proteins, articodies, their derivatives and/or conjugates. They may form part of a piarmaceutical composition to deliver the compound selected from a diagnostic or therapeutic compound, to treat at least one condition such as camer or an infectious disease, or which targets a cancerous cell and to deliver a peptide or inhibitor that its pathogen-infected cell and to deliver a peptide or inhibitor that its armost the activity of the enzyme. The agent of the invention has a transfection efficiency of at least 5% for at least two of the members of the group of the compounds and cell types, has a low toxicity, are a broad spectrum of compounds and cell types, has a low toxicity, are a broad spectrum of pompulate in conjunction with the many different compound types that it can deliver. The peptides are serum sensitive, thus they bode particularly well for systemic and/or localised
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 in patients. The current sequence represents a new amphipathic peptide vector of the invention that contains a cationic nuclear localisation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  vertebrate; therapeutic; tissue imaging;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Delivering agent to target site in vertebrate comprises loading red
is useful for a non-covalent association with and transport of Reterologous compound into a cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .;
O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 23;
5. 0.71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Signal sequence based peptide I MPS peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Pred ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24.28; Score 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human immunodeficiency virus type 1. Roesus macaque polyoma virus.
                                                                                        Example 2; Page 61; 156pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABB81176 standard; peptide: 27 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Red blood cell; RBC; virus;
gp41; memrane translocation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C1-FEB-2001; 2001GB-0C02561.
16-FEB-2001; 2001US-2E9528P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-FEB-2002; 2002WO-GB0C437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity luv...
Nac 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7 LFLGWLGA 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 LFLGWLGA 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mchale AP, Craig R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2002-643355/69.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (GEND-) GENDEL LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200250416-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25-NOV-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      08-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sednesce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A3B81176;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sedneuce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABB81176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C×COOOCCCCCCCCCCCCCXXXAAAA
                    potential therapeutic applications. The polypeptides of the invence of inferential therapeutic applications. The polypeptides of the invence of inferentiation activities; including cytokine, cell proliferation or cell feature activity; activity tissue growth activity; hammatopolesis regulatory activity; tissue growth activity; chammatopolesis regulatory activity; tissue growth activity; immunomodulatory activities; tissue growth activities; chemoteric or chemokinetic activities; hammatory activities; and respect thrombolytic activities; concer cell proliferation or metastasis. Concepted in oncogenesis, cancer cell proliferation or metastasis. Concepted in oncogenesis, cancer cell proliferation or metastasis. Conditions, e.g., by protein or gene therapy. Such conditions include conditions, e.g., by protein or gene therapy. Such conditions include cancers, hemmatopoletic disorders (e.g., myeloid or lymphoid cell disorders or proliferative retinopathy, atherosclerosis, coronary heart disease.

Cancers, chronic inflammatory conditions (e.g., astama or arthrisis), proliferative retinopathy, atherosclerosis, coronary heart disease.

Cancers, chronic inflammatory conditions (e.g., vistoporosis), and abmormat vascular growth. Polypeptides involved with tissue regeneration and vascular growth. Polypeptides involved with tissue regeneration and fungal infections in addition to immune disorders.

Companies them cells in culture to give rise to neuroepithelial cells may also be used in the diagnosis of the above conditions, and in drug companies and not promote of the condiming techniques. The present sequence represents a novel human convergence of the inventing conditions, and indices on promote of the inventing techniques.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ..
O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Intracelluiar delivery; transfection agent; cancer; infectious disease;
        giving an insight into their probable biological activities, and hence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Transfection agent that comprises a peptide comprising hydrophobic and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Heitz F, Fernandez J, Archdeacon J:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 225;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 9; DB 22
Pred. No. 0.62
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABB77688 standard; peptide; 24 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27.
100.08: F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mery J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 polypeptide of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31-JUL-2000; 2000US-221932P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26-JUL-2001; 2001WO-US23406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (ACTI-) ACTIVE MOTIF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JUL-2062 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 27.3
Best Local Similarity 100.
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New peptide vector#4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Morris M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2002-329441/36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12 LGADRFYLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    peptide vector.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200210201-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  07-FEB-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Horndorp K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Divida G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABB77688;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 6
ABB77688
          ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
```

Ö

Gaps

Ċ:

Disclosure; Page 11; 61pp; English.

S

```
us-09-852-100a-2_copy_185_217.rag
```

blood cell with virus or virus-like particle comprising agent, sensitizing cell, introducing cell into vertebrate and applying energy to release virus particle from cell -

Disclosure; Page 55; 87pp; English.

The invention relates to delivering an agent to a target site in a vertebrate. The method involves (a) loading a red blood cell (RBC) with a virus or a virus-like particle (1) comprising an agent; (b) sensitizing RBC to render it more susceptible to disruption than unsensitized RBC; (c) introducing RBC into a vertebrate, and (d) applying energy to release (I). Steps (a) and (b) may be performed in any order. (II) (RBC loaded with a virus or a virus-like particle comprising a therapeutic agent to a larget site in a vertebrate, or in the preparation of a mediament of delivery of a therapeutic agent to a target site in a vertebrate and of also useful for delivering one or more agents to a vertebrate and for treating or preventing a disease. The method is useful for delivering agents such as those useful for imaging of tissues in vivo or ex vivo, preferably for delivering an agent to a subcellular organelle such as nucleus, mitochondria, G5.gi or endoplasmic reticulum. The present sequence represents a signal sequence based peptide: MPS peptide a chimera of the hydrophobic terminal domain of viral ap41 protein and the succiear localisation signal (NLS) from the SV40 large antigen. This fragment has been found to be active in membrane translocation.

27 NA; Seguence

Gaps ö 24.2%; Score 5; DB 23; Length 27; 100.0%; Pred, No. 0.8; 0; Indels tive 0; Mismatches 0; Indels Ouery Match
Best Local Similarity 100.
Matches 8; Conservative 7 LFLGWLGA 14 3 LFLGWLGA 10

្វ

RESULT

ABG78990 standard; Peptide: 27 AA. 15-NOV-2002 (first entry) ABG78990; ABG78990

Cell penetrating peptide Signal-peptide II.

Cell penetrating peptide; cancer; tumour; melanoma; thymoma; lymphoma; sarcoma; iung cancer; non-Hodgkin's lymphoma; leukaemia; Hodgkin's lymphoma; uterine cancer; cervical cancer; bladder cancer; kidney cancer; adenocarcinoma; breast cancer; prostate cancer; ovarian cancer; pancreatic cancer; vaccine; dendritic cell; tumour infiltrating lymphocyte; TIL; human leukocyte antigen; HLA; cytostatic

Unidentified

WO200254057-A2.

22-AUG-2002.

15-FEB-2002; 2002WO-US05212.

5-FEB-2001; 2001US-268687P

(BAYU) BAYLOR COLLEGE MEDICINE.

Wang R;

WPI: 2002-627577/67.

Novel composition for treating a disease in an animal, comprises an immune effector cell and cell penetrating peptide associated with an

Claim 45; Page 44; Slpp; English.

RNA binding domain

```
Ξ
                                                                                                               antibody. Also included are (1) a vaccine comprising (1). Coparation and antigen composition for a disease, by providing (1) and (2) preparing a composition for a disease, by providing (1) and (2) preparing a composition for a disease, by providing (1) and (2) preparing a composition for a disease, and introducing the antigen easociated with an antigen for disease, and introducing the antigen easociated CPP to (1), where antigen enters into the celi. The antigens are, for example, tunnour antigen derived epitopes recognised by tunnour influrating lymphocytes (TIL) of file (buran immunity in an animal to a disease, by administrating a mature dendritic cell comprising CPP associated with an antigen to disease, to the animal comprises both CDH and comprises both CDH and comprises both CDH and COBH T cells. It is also useful for treating a disease (e.g. cancer, tunnour, melanoma, thymoma, lung cancer, non-Hodgkin, simphoma, leukaemia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                              a cancer treatment including surgery, radiation, chemotherapy or gene therapy. The administration of (I), preferably dendritic cell is prior to, subsequent to or concurrent with, the cancer treatment. The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Quantifying target gene expression in living cells that possess a target gene of interest tagged with the binding site for an RNA binding protein and fluorescently labeled RNA binding polypeptide including an
                                                                               The invention relates to a composition (I) comprising an immune effector cell and a cell penetrating peptide (CPP) associated with an antigen or
                                                                                                                                                                                                                                                                                                                                                                                                 Hodakin's lymphoma, uterine cancer, cervical cancer, bladder cancer, kidney cancer, adenocarcinoma, breast cancer, prostate cancer, ovarian cancer and pancreatic cancer). The animal is further subjected
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .;
O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RNA binding protein; mRNA quantification; gene expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24.2%; Score 8; DB 23; Length 27; 100.0%; Pred. No. 0.8; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequence is cell penetrating peptide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fluorescently labelled RNA binding peptide #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAE23685 standard; peptide; 27 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-SEP-2001; 2001WO-US30438.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28-SEP-2000; 2000US-236407P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 100.
es 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (CETT-) CETTOWICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7 LFLGWLGA 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 LFLGWLGA 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2002-452280/48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200227031-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10-SEP-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 04-APR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAE23685;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Busa WB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAE23685
```

```
The present invention relates to a method of quantifying the expression of target genes in living cells. The method involves providing cells that possess a target gene of interest which has been tagged with the binding site for an RNA binding protein and a fluorescently labelled RNA binding protein and a fluorescently labelled RNA binding polypeptide that includes an RNA binding domain and calculating the quantity of target gene expression in the cells using fluorescence signalling techniques. The method is useful for quantifying expression of one or more target genes in living cells which comprise two or more distinct populations of cells. It is used to quantifate the expression of any target gene, including expression of protein-encoding messenger. RNA genes, ribosomal RNA encoding genes and transfer RNA encoding qenes so long as the RNA expression product from the target gene possesses a sequence or structure (the RNA tag) that is bound specifically by the RNA binding polypeptide being used. The present sequence is a fluorescently labelled RNA binding peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Intracellular delivery; transfection agent; cancer; infectious disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24.2%: Score 8; DB 23; 100.0%; Pred. No. 0.8; ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABB77687 standard; peptide; 27 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JUL-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.
Matches 8: Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New peptide vector#3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7 LFESWLGA 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 LFLGWLGA 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                            27 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      peptide vector.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABB77687;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABB77687
a
```

٠. ن

Gaps

ö

Length 27; 0; Indels

```
Misc-difference 23
             Misc-difference 7
          Synthetic
```

/notes "residue may be substituted with Ser" /note= "residue may be substituted with Phe" Location/Qualifiers

WO200210201-A2

07-FEB-2002

26-JUL-2001; 2001WO-US23406

31-JUL-2000; 2000US-221932P

(ACTI-) ACTIVE MOTIF.

Archdeacon 3; Fernandez J, Heitz F, Mery J, Morris M, Horndorp K; Divida G,

WPI; 2002-329441/36.

Transfection agent that comprises a peptide comprising hydrophobic and hydrophilic domain and having amino acid residues of specified length is useful for a non-covalent association with and transport of a heterologous compound into a cell

Example 2; Page 61; 156pp; English

The invention relates to a transfection agent comprises a peptide of

```
Ġ
                                                                                                                                                      diagnostic or therapetics compound, to treat at least one condition such as cancer or an infectious disease, or which targets a cancerous cell or pathogen-infected cell and to deliver a poptide or inhibitor that disrupts the activity of the enzyme. The agent of the invention has a transfection efficiency of at least 5% for at least two of the members of a broad spectrum of compounds. The agent has a good delivery efficiency for a broad spectrum of compounds and cell types, has a low toxicity, are easy to handle and easy to formulate in conjunction with the many sensitive, thus they bede particularly well for systemic and/or iocalised in patients. The current sequence represents a new amphiputhic peptide vector of the invention that contains a calionic nuclear localisation
           a hydrophobic domain, a hydrophilic domain, optionally a spacer sequence between the domains and a functional group conjugated to at least one terminal of the peptide. Peptides of the invention are useful for a non-covalent association with and transport of a heterologous compound into a cell. They are also useful for promoting the cellular artibodies, their derivatives and/or conjugates. They may form part of a harmaceutical composition to deliver the compound selected from a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Proparing a red blood cell vehicle suitable for delivering an agent to a target site in a vertebrate due to loading the red blood cell with an agent-membrane translocation sequence -
- 30 amino acids in length. Peptides of the invention comprise
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Membrane translocation signal; signal sequence based peptide 1; red blood cell vehicle; polypeptide delivery; viral gp41 protein; simian virus 40; SV40; large antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                24.2%; Score B; DB 2
100.0%; Pred. No. 0.8
Live 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure: Page 44; 135pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAU78348 standard; Peptide; 27 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Signal sequence based peptide I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rhesus macaque polyoma virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24-JUL-2030; 2000WO-GB02848.
C9-AUG-2030; 2000WO-GB63056.
01-FEB-2001; 2001WO-GB00417.
16-FEB-2001; 2001US-0785802.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24-JUL-2001; 2001WO-GB03327
                                                                                                                                                                                                                                                                                                                                                                                                                             Guery Match
Best Local Similarity 10v.v.
Best Local Similarity 10v.v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7 LFLGWLGA 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 LFLGWLGA 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2002-280593/32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (GEND-) GENDEL LTD
                                                                                                                                                                                                                                                                                                                                                                                                              27 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         W0200207752-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24-JUL-2000; 209-AUG-2000; 201-FEB-2001; 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31-JAN-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAU78348;
                                                                                                                                                                                                                                                                                                                                                                                                                  Sednence
                                                                                                                                                                                                                                                                                                                                                                              seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Craig R:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAU76348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           e.
```

```
ö
         The invention describes a method of preparing a red blood cell vehicle suitable for delivering an agent to a target site in a vertebrate comprising providing a red blood cell and loading the red blood cell with an agent-WTS (membrane translocation sequence) conjugate. The red blood cells produced may be used in the preparation of a medicament for delivery of an agent to or at a target site and of one or more agents to a vertebrate. The agent is actively released from the red blood cell vehicle by application of a stimulus to disrupt the red blood cell vehicle. This sequence represents signal sequence based peptide 1. a chimeric peptide of the hydrophobic terminal domain of the viral gp41 protein and the nuclear localisation signal from simiar virus 40 (SV40) large antiger, one of the membrane translocation peptides tested
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MTS; membrane translocation sequence; plasma membrane; red blood cell; immunisation; antigen; intracellular delivery; therapeutic: HIV-1; trans-activating protein; Tat; Antenapedda nomeodomain protein; Antp-HD; VP22 protein; HSV-VP22; signal-sequence-based peptide; Tranportan; NLS; Amphiphilic model peptide; SV40; Simian virus 40; qp41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Translocation; delivery vehicle; agent-membrane translocation sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Preparing delivery vehicles, particularly red blood cells, for the intracellular delivery of a therapeutic agent to a target site, by loading a cell with an agent-MTS conjugate, which comprises a membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention discloses a method for preparing a delivery vehicle for delivering an agent to a target site in a vertebrate. The method
                                                                                                                                                                                                                                               Cars
                                                                                                                                                                                                                                               .;
                                                                                                                                                                                                                    24.2%; Score 8; DB 23; Length 27; 100.0%; Pred. No. 0.8;
                                                                                                                                                                                                                                               0; indels
                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  - Rhesus macaque polyoma virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 8; 43pp; English.
                                                                                                                                                                                                                                                                                                                                                              ABG75506 standard; Peptide; 27 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                         Signal-sequence-based peptide I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              nuclear localisation sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2000GB-0602848.
2000GB-0003056.
2000US-0748063.
2000US-0748789.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-FEB-2001; 2001US-0785802
                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                 Query Match
Best Local Similarity 190.
Matches 8: Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    translocation sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chimeric - Viruses sp
                                                                                                                                                                                                                                                                                    1111:111
3 LFLGWLGA 10
                                                                                                                                                                                                                                                                      7 LFLGWLGA 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2003-182503/18
                                                                                                                                                                                            27 AA;
                                                                                                                                                                    in the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US2002151004-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (CRAI/) CRAIG R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                09-AUG-2000;
22-DEC-2000;
22-DEC-2000;
                                                                                                                                                                                                                                                                                                                                                                                                               14-APR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24-JUE-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17-0CT-2002
                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                       ABG75506;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chimeric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Craig R;
                                                                                                                                                                                                                                                                                                                                      RESULT 12
                                                                                                                                                                                                                                                                                                                                                                          X 000000000000000X8
                                                                                                                                                                                                                                                                                              pp
```

```
comprises loading a cell with an agent-membrane translocation sequence carbonings the agent to cross the plasma membrane of a cell. Also disclosed can abling the agent to cross the plasma membrane of a cell. Also disclosed is a pharmaceutical composition comprising a red blood cell for delivery correctly and a method of immunisation of an animal with an anticularly a red blood cell, for the intracellular delivery of a chiquenty a red blood cell, for the intracellular delivery of a therapeutic agent to a target site. The method is particularly useful for preparticularly a red blood cell, for the intracellular delivery of a therapeutic agent to cross the plasma membrane of a target cell, and for selectively releasing the agent by the cells at the target site to facilitate the uptake of the agent by the cells at the target site. The cellitate dMTS sequences are from HIV-1 trans-activating protein (fat), brosophila Antennapedia homeodomain protein (Antp-HD), Herpes Simplex-1 brosophila Antennapedia homeodomain protein (Antp-HD), Herpes Simplex-1 crimanopertan and Amphiphilic model peptide. The sequence presented is the Signal-sequence-based opptide I, which comprises the hydrophobic terminal chambin the Viral gp41 protein and the nuclear localisation sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Red blood cell; transgenic; cytostatic; immunosuppressive; SV40; MPS; antificumatic; antiartbritic; dermatological; antithyroid; noctropic; neuroprectective; carebropretective; carediant; artifarthythmic; litholytic; antiinflammatory; nephrotropic; antidabetic; antiasthmatic; vinerary;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Producing red blood cells for polypeptide delivery, by obtaining a red blood cell containing the polypeptide from a transgenic animal expressing a gene encoding the polypeptide, and sensitizing the cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24.2%; Score B; DB 24; Length 27; 100.0%; Pred. No. 0.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           :0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Signal sequence based peptide I MPS peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABB82542 standard; peptide; 27 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2001US-264808P.
2001WO-GB00417.
2001US-0785802.
2001GB-0005631.
2001US-279803P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 analgesic; osteopathic; gp41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rhesus macaque polyoma virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16-JAN-2002; 2002WO-GH00169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2001WO-GB03327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 100.
Matches 8: Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Craig RK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7 LFLGWLGA 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2003-040499/03.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GEND-) GENDEL LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    W0200257436-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29-JAN-2001;
01-FEB-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16-FEB-2001;
07-MAR-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24-531-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29-MAR-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        04-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            McHale AP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABB82542;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A5582542
```

ID NO 22500; 21pp + Sequence Listing; English

```
Disclosure; SEC
                                                                                                                                                                                            Sednence
                                                                           cell-cell
                                                                                                                                                                                                                                                                                                                                                                                     AAY70751;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Domain
                                                                                                                                                                                                                                                                                                                                               AAY70761
                                                                                                                                                                                                                                                                                                                                                                          a
                                                                                                                                                                                                                                                                       õ
                                                                                              d rea blood cell controlling the Porperior and annual and an annual and a rea blood cell controlling the red blood cell controlling the red blood cell produced by or obtainable from the method is useful for inearing cell produced by or obtainable from the method is useful for inearing diseases including cancer, non-mailtainable from the method is useful for inearing cutoimmune disorders (e.g. rheumatoid arthritis, inpus crythematosus. Coraves's disease) muscular disorders (e.g. rheumatoid arthritis, inpus crythematosus. Coraves's disease), neuromiscular disorders (e.g. amyotrophic lateal scletosis and others), neuromiscular disorders (e.g. blood others), neuromiscular disorders (e.g. blood others), neuromiscular disease. Coretrai or venous disease (e.g. blood others or other arterial/venous blockage, such as from cholestrool or amyloid deposition), liver disease (e.g. cirrhosis), read disease (e.g. plood others or other arterial/venous polypeptide is also useful in the treatment of injury, inflammation, burns, carped tunnel syndrome or codultions resulting from hijury, such as osteoarthritis. The present sequence represents a MPS peptide (signal sequence derived peptide 1), a chimera of the wiral gold protein and the nuclear localisation signal sequence (NLS) from the SV40 large antigen. This has been found to be active in
                                                                                                                                                                                                                                                                                                                                                                                                              ::
:
                                                The invention relates to producing a red blood cell suitable for delivery of a polypeptide to a vertebrate, by providing a transperie animal carrying and expressing a transpers encoding the polypeptide, obtaining a red blood cell containing the polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New isolated nucleic acid detection reagent for detecting 10% or more genes from Drosophila and for elucidating cell signaling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                    DB 24; Length 27: . 0.8;
                                                                                                                                                                                                                                                                                                                                                                                                               0; Indeis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Drosophila melanogaster polypeptide SEQ ID NO 22500.
                                                                                                                                                                                                                                                                                                                                                                                    Score 8; DB 24; Pred. No. 0.8; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Myers EW;
                         Disclosure: Page 50; 125pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABB65236 standard; Protein; 178 AA.
                                                                                                                                                                                                                                                                                                                                                                            24.28; SCC.
100.08; Pre
0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PWD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23-MAR-2000; 2000US-191637P.
11-JUL-2000; 2000US-0614150.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23-MAR-2001; 2001WO-US09231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ξ
                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 100.
nes 8, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                     membrane translocation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Venter JC, Adams M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                      LFLGWLGA 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-656860/75.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (PEKE ) PE CORP NY
                                                                                                                                                                                                                                                                                                                                                             27 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; ABL09339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200171042-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 interactions -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             pharmaceutical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABB65236;
                                                                                                                                                                                                                                                                                                                                                              Sedneuce
                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                 Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABB65236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            q
```

```
9
                                7.8
                                                                                                                                                                                                        The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                             invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           beta-amyloid peptide blading protein; BBP; BAP; timour; suppressor;
G-protein coupled receptor; GPCR; integral membrane protein; antigen;
nouronal cell; nonhuman primate; NHP; G-protein signalling pathway;
apoptosis; immunogen; therapeutic; treatment; prevention; diagnostic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /label- DRF_motif
/note= "Substitution of the Arg abrogates protection"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel G-protein-coupled receptor-like proteins and polynucleotides useful for regulating apoptosis, comprises integral membrane protein traversing the membrane twice
                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The inventiuseful in developmental biology and in elucidating cell signalling a
                                                                                                    insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
                                                                                 interactions in higher eukaryotes for the development of
                                                                                                                                                                                                                                                                                                                                                                                                                    .:
                                                                                                                                                                                                                                                                                                                                                                Length 178;
                                                                                                                                                                                                                                                                                                                                                                                                                    0; lndels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human beta-amyloid peptide (BAP) binding protein, BBP3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /label- Transmembrane_domain_l
176..178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /label- Transmembrane_domain_2
                                                                                                                                                                                                                                                                                                                                                                   DB 22;
                                                                                                                                                                                                                                                                                                                                                     24.2%; St. 100.0%; Pred. No. 7. 100.0%; Pred. No. 7. 100.0%; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 1; Page 67-68; 68pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY70761 standard; Protein; 221 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ្ន
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (AMHP ) AMERICAN HOME PROD CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kajkowski EM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98US-0104164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                          Guery Match
Sest Local Similarity 160...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ..178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     108 DRFYLGYP 115
                                                                                                                                                                                   (ABB57737-ABB72072).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15 DRFYLGYP 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI: 2000-317982/27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; AAZ52371.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WC200022125-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ozenberger BA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13-0CT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13-CCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24-JUL-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20-APR-2000
```

```
The present sequence is the beta-amyloid peptide (bAF) binding protein. (BBP3). It is an integral membrane protein, that traverse the membrane by the confidence of GPF) protein subject (GPF) protein superfamily. It interacts with G-alpha proteins and regulates the activity of G-protein signalling pathways. BBP genes are widely expressed in neuronal cells of nonhuman primate (NFP) brain and overexpressed in some tumours. It functions as a suppressor of apoptosis induction. SBP proteins are used as immunogens to raise antibodies, useful as therapeutics and as autiques in solid phase assays. They are also useful as reagents to identify molecules which effect the interaction of SBP and a cloned protein, that are useful in the treatment or prevention of diseases associated with apoptosis. The polyncieotides are useful tor
      8×399999999998×8
```

221 AA; Sequence

Query Match 24.2%; Score 8; DB 21; Length 221; Best Local Similarity 100.0%; Pred. No. 5.7; Matches 8; Conservative 0; Mismatches 0; Indels

ö

Gaps

..

Search completed: September 26, 2003, 17:39:25 Job time : 17.7106 secs

13 GADRFYLG 20

QC οy

```
5.1.6
Compugen Ltd.
GenCore version Copyright (c) 1993 - 2003
```

using sw model - protein search, OM protein September 26, 2003, 17:36:55 : Search time 5.89787 Seconds (Without alignments) 236.739 Million cell updates/sec Run on:

US-09-852-100A-2_COPY_185_217

1 VAVALSLFLGWIGADRFYLGYPALGLIKFCTVG 33 Title: Perfect score: Sequence:

OLIGO Gapop 60.0 , Gapext 60.0 Scoring table:

328717 seqs, 42310858 residues Searched:

0 Word size

328717 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 6 Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Issued_Patents_AA:* Database :

1: /cun2_6/ptodata/i/laa/5A_COMB.pep:*
2: /cgn2_6/ptodata/i/laa/5B_COMB.pep:*
3: /cgn2_6/ptodata/i/laa/5A_COMB.pep:*
4: /cgn2_6/ptodata/i/laa/6B_COMB.pep:*
5: /cgn2_6/ptodata/i/laa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/i/laa/PCTUS_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	* Query Match	Jength	DB	1D	Description	
-1	æ	24.2	358		US-09-411-628-11	Sequence 11	Appl
7	7	Ϊ.	451	÷	US-09-345-47 1E-45		, Appl
m	7	ij	462	₹	US-09-328-352-6899		188, Ar
4	7	21.2	483	~5	-25		29267. A
L(r)	7	Ξ.	617	٠.	-09-345-473E-4		, App.
φ	9		46	7	-486-		131. App
7	9			4	-08-508-	•	
80	9			٣	-905-223-	Sequence 314	.4. Apr
6	9			4	-486-		
10	9			4	-228-986-11		
11	9			~	-675-508	Sequence 2,	App.
12	9			٣	US-39-203-939-2	Sequence 2,	App. :
13	9			m	9-203-	Sequence 6,	Appl
14	9			٣	US-09-251-835-2	Sequence 2,	Appli
15	9			~	5	Sequence 6,	App.:
16	9			٣	US-09-318-503-2	Sequence 2,	App1:
17	9			~	9-318-	Seguence 6,	Appli
18	9			m	US-09-038-261A-2	Sequence 2,	App
19	9	18.2		m	US-09-038-261A-6	Sequence 6,	Appli
20	9			4	64-3	Sequence 2,	App. i
21	9			4	64-3		Appl:
22	9			7		Sequence 31,	Appl
23	9		~	ಶ	52-		1349, A
24	9		7	4	52-991A-3		33042, A
25	9		325	4	-09-252-		16657, A
56	9		c	4	-09-162-	m	Appii
27	9		350	4	US-08-637-670-25	25	, Appl

21.2%; Score 7; DB 4; Length 451; 100.0%; Pred. No. 21;

Ouery Match Best Local Similarity

6 18.2 380 4 18.2 18.2 380 4 18.2 389 4 1 18.2 389 4 1 18.2 389 4 1 18.2 389 4 1 18.2 389 6 4 18.2 389 6 4 18.2 389 6 4 18.2 389 6 4 18.2 389 6 4 18.2 389 6 6 18.2 4 32 1 18.2 380 6 6 18.2 4 32 1 18.2 380 6 6 18.2 4 33 4 1 18.2 4 33 4 1 18.2 6 18.2 6 6 6 18.2 6 6
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~

### ALIGNMENTS

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ö
          US-09-411-628-12
Sequence 11, Application US/09411628
Faton No. 6428994
FATOR NO. FATOR SEQUENCES OF THE PRODUCTED PROTEIN
TITLE OF INVENTION: CDN., GENOMIC, AND PREDICTED PROTEIN
TITLE OF INVENTION: SEQUENCES OF LEARNING-INDUCED KINASES
FILE REFERENCE: 13761-707
CURRENT PILING DATE: 1999-10-01
FARIJER APPLICATION NUMBER: US 60/102, 906
FARIJER FILING DATE: 1998-10-02
FARIJER FILING DATE: 1998-10-02
FOUNDER OF SEQ ID NOS: 16
SOFTWARE: FASTSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 45, Application US/09345473E
Sequence 45, Application US/09345473E
Sequence 45, Application US/09345473E
Sequence 45, Application US/09345473E
SEMERAL INFORMATION:
APPLICANT: Hodge, Martin
TITLE OF INVENTION: No. 6558903el Kinases and Uses Thereof
TITLE OF INVENTION: No. 6558903el Kinases and Uses Thereof
CURRENT APPLICATION NUMBER: US/09/345,473E
CURRENT FILING DATE: 1999-06-30
NUMBER OF FILING PATE: 1999-06-30
SOFTWARE: FASTERO for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cucry Match
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 8; Conservative 6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    : ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11111111
259 YPALGLLK 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21 YPALGLLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-345-473E-45
                                                                                                                                                                                                                                                                                                                                                                                        SEC ID NO 11
LENGIH: 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQ ID NO 45
LENGTH: 451
                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 2
RESULT 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       a
C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ð
```

٠,

us-09-852-100a-2_copy_185_217.rai

N

:

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                       ó
                                                                                                                                                                                                                                         Length 617;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                       indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: YOUNG et al.
TITLE OF INVENTION: 207 Human Secreted Proteins
FILE OF INVENTION: 207 Human Secreted Proteins
FILE OF INVENTION NUMBER: US/09/205,258
CURRENT FILING DATE: 1998-12-04
EARLIER APPLICATION NUMBER: PCT/US/98/11422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        : LOCATION: (46)
: OTHER INFORMATION: Xaa equals stop translation US: 09-489-8847-131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18.2%; Score 6; DB 4; 100.0%; Pred. No. 25;
                                                                                                                                                                                                                                       21.2%; Score 7; DB 4; 100.0%; Pred. No. 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Rosen et al TILLE OF INVENTION: 98 Human Secreted Proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/489,847
CURRENT APPLICATION NUMBER: US/09/489,847
CURRENT FILING DATE: 200-01-24
EARLIER APPLICATION NUMBER: PCT/US9/17130
EARLIER FILING DATE: 1998-07-29
EARLIER APPLICATION NUMBER: 60/095,486
EARLIER APPLICATION NUMBER: 60/095,486
EARLIER APPLICATION NUMBER: 60/095,486
EARLIER FILING DATE: 1998-08-05
EARLIER FILING DATE: 1998-08-05
EARLIER FILING DATE: 1998-08-05
EARLIER FILING DATE: 1998-08-06
SOFTWARE: PALENT NOWER FILING DATE: 1998-08-06
SOFTWARE: PALENT NOWER FILING DATE: 1998-08-06
SOFTWARE: PALENT NOWER FILING DATE: 1998-08-06
NUMBER OF SEQ ID NOS: 376
SEC ID NOS: 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                    0; Mismatches
CURRENT APPLICATION NUMBER: US/09/345,473E CURRENT FILING DATE: 1999-06-30 NUMBER OF SEQ ID NOS: 62 SOFTWARE: FastSEQ for Windows Version 4.0 JENGTH: 617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 298, Application US/09205258
Patent No. 6525174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Segmence 131, Application US/09489847
Patent No. 6475195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6; Conservative
                                                                                                                                                                                                                                                                                       7; Conservative
                                                                                                                                          TYPE: PRT
CRGANISM: Mus musculus
US-09-345-473E-44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CRGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                  | ||||||||
582 ALSLFLG 588
                                                                                                                                                                                                                                                                                                                                      4 ALSEFEG 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Bost Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24 LGLLKF 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1C LGLLKF 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 7
US-09-205-258-298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 72-09-489-847-131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRI
                                                                                                                                                                                                                                         Clery Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8
                                                                                                                                                                                                                                                                                                                                         55
                                                                                                                                                                                                                                                                                                                                                                                 0.0
                                                                                                                                                                                                                                                           SENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUNANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 5888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: MAIC J. RUBERFIELD AND AMINO ACID SEQUENCES RELATING TO PSEUDDMCNAS TITLE OF INVENTION: MUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDDMCNAS TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS.
FILE REPERENCE: 107196.136
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR PLING DATE: 1998-07-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ë
     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      <u>ن</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0
     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 462;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 483;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Hodge, Martin
TITLE OF INVENTION: No. 6558933el Kinases and Uses Thereof
FILE REFERENCE: 35800/183781
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
       indels
     ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21.2%; Score 7; DB 4;
100.0%; Pred. No. 23;
tive 6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 21.2%; Score 7; 55 4; Best Local Similarity 100.0%; Pred. No. 22; Matches 7; Conservative 0; Mismatches
     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 29267, Application US/09252991A Patent No. 6551795
                                                                                                                                                                                                                   Sequence 6888, Application US/09328352 Patent No. 6562958
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 5
US-09-345-473E-44
: Sequence 44, Application US/09345¢73E
; Patent No. 6558903
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; ORGANISM: Acinetobacter baumannii
US-09-328-352-6888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pseudomonas aeruginosa
     .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 21.3
Best Local Similarity 100.
Matches 7; Conservative
  7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        334 ALSLFLG 34C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   438 PALGLLK 444
                                                                                416 ALSLFLG 422
                                                  4 ALSLFLG 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 ALSLFLG 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22 PALGLEK 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-252-991A-29267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-252-991A-29267
                                                                                                                                                                                               US-09-328-352-6898
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                               qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            a
                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               03
```

ö

us-09-852-100a-2_copy_185_217.rai

1998-06-04	BER: 00/048, 97-06-06	R: 60,	BER: 60	NUMBER: 6	NUMBER: 60	NUMBER: 60	1997-06-0 NUMBER: 60,	1997-NUMBER	1997-06-06	NUMBER: 6	NUMBER: 60	NUMBER: 60	1997-06-0 NUMBER: 60	1997-06-06 NINGER: 60.049 99	1997-06-0	NUMBER: 60	NUMBER: 60	97-06-0 988-06-0	97-06-06	NUMBER 1997-	SR: 50	00-0 SR: 60	7-06-06	06 - 06	28: 60,	SR: 60	06-60 1.660	7-05-1 SR: 6	7-06-06	7-06-06	JR: 6	3R: 6		- 00 - SR: 6:	1997-06-06 IMRFR: 60.7048.8	1997-06-06	NUMBER: 60/048,897 : 1997-06-06	NUMBER: 6	997-06-1 MBER: 61	90-90-266	NUMBER: 60/048,963 : 1997-06-06	NUMBER: 6	9	90-16
LING	LICALL ING DA	LICALI	LICATI	APPLICATION FILLING DATE:	LICATION	LICATION	ING DA	ING	ING DA	LICATION	LICATION	LICATION	HNG DAI	ING DATE	ING DATE	LICATION	LICATION	LING DATE	ING DATE	LICATION	LICATION	LICATION	ING DATE	ING DATE	LICATION	LICATION	ING DATE	ING DATE	LING DATE	ING DATE	LICATION ING DATE	SICATION	LICATION	LING DAIR	ING DA	ING DA	LICATION	PPLICATION	出る	LING DATE	PLICATION LING DATE	PLICATION	4	ILING DAT
R E	ARLIE	ARLI	ARLI	3 2 2	ARLI	ARLI	ARLII ARLII	ARLI	ARLI	ARL ARL	ARLI PT		ARLI ARLI	ARLI	ARLI	ARLI	RLI	ARLI	ARLI	ARLI ARI.I	ARLI	15	5.	; ;	11	1 1	EARLIER EARLIER	7.5	3.	1	ᄪ	7.	ARLI	ARLI		ARLI	: EARLIER	ARLI	HH	ARLIE	R.L.		Z.	RLIE

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                      .
O
                                                                                                                                                                                                                                                                                                                                                                          Query Match 18.2%; Score 6; DB 4; Length 70; Best Local Similarity 100.0%; Pred. No. 37; Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 8
US-08-305-223-314
Sequence 314, Application US/08905223
Fatent No 6222029
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Edwards, Joan-Baptiste D.
APPLICANT: Lacroix, Bruno
ITLE OF NUMBER OF SEQUENCES: 503
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Wartens, Olson & Bear
SIREF: San Diego
CITY: San Diego
CITY: San Diego
SIATE: California
                                                                                                                                                                                                                                                 FEATURE:
NAME/KBY: STTE
LOCATION: (70)
COTHER INFORMATION: Xaa equals stop translation
US-05-205-258-298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MAMEKEY: sig_peptide
LOCATION: -42...1
IDENTIFICATION METHOD: Von Heijne matrix
EARLIER APPLICATION NUMBER: 60/070,923
EARLIER FILING DATE: 1997-12-18
EARLIER PRPLICATION NUMBER: 60/092,921
EARLIER FILING DATE: 1998-07-15
EARLIER FILING DATE: 1998-07-15
EARLIER FILING DATE: 1998-07-15
EARLIER FILING DATE: 1998-07-30
NUMBER OF SEQ ID NOS: 1227
SOFTWARE: PATENTIN VGT: 2.0
SEQ ID NC 298
LENGTH: 70
TYPE: PAT
CREANIEM: HOMO SAPIENS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CONTRY: USA

ZIP: 92101-3505

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC COMpatible
OPERATING SYSTEM: Win95
SOFTWARE: Word
CURRENT APPLICATION DATA:
RPLICATION NUMBER: US/08/905,223
FLING DATE:
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY AGENT INFORMATION:
NAME: Israelsen, Ned A.
REGISTATION UNDRER: 29,655
REFERENCE/DOOKET WINNER:
TELECOMMUNICATION INFORMATION:
TELEFAX: (619) 235-0176
INFORMATION FOR SED ID NO: 314:
SEGUENCE CHARACTERISTICS:
LENGIH: 72 annio acids
TYPE: AMIO ACID
TOPOLOGY: LINEAR
MOLECULE TYPE: PROTEIN
ORIGINAL SOURCE:
OREGNISM: HOMO Sapiens
TISSUE TYPE: Brain
                                                                                                                                                                                                                                                                                                                                                                                                                                                          ŝ
```

: ٔ

0

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Reiter, Robert E.
APPLICANT: Witte, Owen N.
TITLE OF INVENTION: PSCA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF
FILE REFERENCE: 30435.540151
CURRENT APPLICATION NUMBER: US/09/203,939
CURRENT FILING DATE: 2000-12-02
PRIOR PELING DATE: 1997-03-10
PRIOR FILING DATE: 1997-03-10
PRIOR FILING DATE: 1997-03-10
                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ..
                                       3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 123,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                         Indels
                                                                                                                                                                                                                                                                        APPLICANT: Au-Young, Janice
TTLE OF INVENTION: NOVEL HUMAN STEM CELL ANTIGENS
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
                                       .,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18.2%; Scor.
100.0%; Pred. No. co.
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 2;
                    Pred. No. 60;
                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Incyte Pharmaceuticals, Inc
STREET: 3174 Porter brive
CITY: Palo Alto
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: U.S.

ZIP: 94304
COUNTRY: U.S.
ZIP: 94304
COMPUTER: EDISKETTE
MEDIUM TYPE: DISKETTE
OFRATING SYSTEM: DOS
SOFTWARE: FASTSEQ VETSION
SOFTWARE: FASTSEQ VETSION
APPLICATION NUMBER: US/08/675,508
FILING DATE: Filed Herewith
ATTORNEY/AGENT INFORMATION:
NAME: BILINGS, LUCY J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: 96,749
TELECOMMUTCATION INFORMATION:
TELEPHONE: 415-85-0555
INFORMATION FOR SEQ ID NO: 2:
SPONEWAT CHARBATERICATIOS.
100.08; Pre
                                                                                                                                                                                              08-06-675-508-2
Seguence 2, Application US/08675508
Patent No. 5856136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 : Sequence 2, Application US/09203939; Patent No. 6258939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 123 amino acids
IYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Guery Match
Bost Local Similarity 100.0
                  Best Local Similarity 130.
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      111 PALGLE 116
                                                                                                    37 VAVALS 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22 PALGLL 27
                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                               1 VAVALS 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IMMEDIATE SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; CLONE;
US-08-675-508-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              38-09-203-939-2
                                                                                                                   9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ad
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Strabala, Timothy
APPLICANT: Strabala, Timothy
APPLICANT: Strabala, Timothy
APPLICANT: Strabala, Timothy
APPLICANT: Nieuwenhuizen, Nieis
TITLE OF INVENTION: Compositions Isolated from Plant Cells
TITLE OF INVENTION: Compositions of Their Use in the Modification of Plant Cell Signalling;
FILE REFERENCE: 11000/1020
CURRENT APPLICATION NUMBER: 15/99/228,986
CURRENT APPLICATION NUMBER: 1999-01-12
NUMBER OF SEQ ID NOS: 130
SOFTHARE: FastSEQ for Windows Version 3.0
SEQ ID NO 111
LENGTH: 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0
                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0
                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 4; Length 117;
                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C; Indels
                                                                                              Length 72;
                                                                                                                                                                                                                                                                                                       Sequence 306, Application US/09489847

Patent No. 6476195

GENERAL INFORMATION

GENERAL INFORMATION

GENERAL INFORMATION

TITLE OF INVENTION: 98 Human Secreted Proteins

TITLE OF INVENTION: 98 Human Secreted Proteins

CURRENT APPLICATION NUMBER: US/09/489, 847

CURRENT FILING DATE: 2000-01-24

CURRENT FILING DATE: 1999-07-29

EARLIER FILING DATE: 1999-07-29

EARLIER PILING DATE: 1999-07-29

EARLIER APPLICATION NUMBER: 60/095,486

EARLIER APPLICATION NUMBER: 60/095,486

EARLIER APPLICATION NUMBER: 60/095,486

EARLIER PILING DATE: 1998-08-05

EARLIER PILING DATE: 1998-08-06

SEQ ID NOS: 376

SEQ ID NO 306

LENGTH: 101
                                                                                              DB 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 6; DB 4;
Pred. No. 52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18.2%; Stor.
100.0%; Pred. No. ...
                                                                                              Query Match 18.2%; Score 6: DB 3
Best Local Similarity 100.0%; Pred. No. 38:
Matches 6: Conservative 0: Mismatches
                                       seq DLAVALSLLPAWT/ES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18.2%; Score 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 111, Application US/09228986
: Patent No. 6359198
: GENERAL INFORMATION:
                score 6.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: PRT
; ORGANISM: Pinus radiata
US-09-228-986-111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Homo sapiens
                                   ; OTHER INFORMATION: US-08-905-223-314
                OTHER INFORMATION:
                                                                                                                                                                                                               32 AVALSL 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           89 AVALSE 94
                                                                                                                                                                         2 AVALSL 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 AVALSI. 7
                                                                                                                                                                                                                                                                                             US-09-489-647-306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-489-847-306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-228-986-111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      δō
```

ö

```
Ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ·:
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18.2%; Score 6; DB 3; Length 123; 160.0%; Pred. No. 63; 0; Indels ivc 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 3; Length 123; ). 63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Reiter, Robert E.
APPLICANT: Mitte, Owen N.
ITILE OF INVENTION: PSCA: PROSTATE STEM CELL ANTIGEN
ITILE OF INVENTION: PSCA: PROSTATE STEM CELL ANTIGEN
FILE REFERENCE: 30435 540512
CURRENT APPLICATION NUMBER: US/09/251,835A
CURRENT FILING DATE: 1999-02-17
PRIOR APPLICATION NUMBER: 66/07:141
PRIOR APPLICATION NUMBER: 66/07:141
PRIOR APPLICATION NUMBER: 66/074,675
PRIOR APPLICATION NUMBER: 09/039,261
PRIOR APPLICATION NUMBER: 09/039,261
PRIOR APPLICATION NUMBER: 09/039,261
PRIOR APPLICATION NUMBER: 09/039,399
PRIOR FILING DATE: 1998-03-10
PRIOR APPLICATION NUMBER: 09/039,939
PRIOR FILING DATE: 1998-12-02
  FILE REFERENCE: 30435.54USI2
CURRENT APPLICATION NUMBER: US/09/251,835A
CURRENT FILING DATE: 1999-02-17
PRIOR APPLICATION NUMBER: 03/814,279
PRIOR FILING DATE: 1997-03-10
PRIOR RILING DATE: 1998-01-12
PRIOR APPLICATION NUMBER: 60/071,141
PRIOR RILING DATE: 1998-02-13
PRIOR FILING DATE: 1998-02-13
PRIOR FILING DATE: 1998-03-10
PRIOR FILING DATE: 1998-03-10
PRIOR FILING DATE: 1998-12-02
PRIOR FILING DATE: 1998-12-02
PRIOR FILING DATE: 1998-12-02
SECONTAINE DATE: 1998-12-03
SECONTAINE: PARTICATION VET: 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18.2%; Score 6; DB 3
100.0%; Pred. No. 63;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 6, Application US/09251835A Patent No. 6261789
                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: HUMAN PSCA (hPSCA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : TYPE: PRT
; ORGANISM: HUMAN PSCA (hPSCA)
US-39-251-835-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19.2
Best Local Similarity 100.
Matches 6; Conservativo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 100.
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION: (50)..(64)
NAME/KEY: SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      111 PALGLL 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22 PALGLL 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22 PALGLL 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Pat
SEQ ID NO 6
LENGTH: 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-251-835-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ċ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .;
O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 6, Application US/09203939
Sequence 6, Application US/09203939
Sequence 6, Application US/09203939
Sequence 6, Application US/09203939
Sequence 6, Application C528939
Sequence 6, Application C528939
APPLICANT: Witte, Owen N.
TITLE CF INVENTION: PSGA: PRCSTATE STEM CELL ANTIGEN AND USES THEREOF FILE REFERENCE: 30435-546S1.
CUBRENT FILING DATE: 2060-22-02
PRIOR PPLICATION NUMBER: 06/071,141
PRIOR FILING DATE: 1997-03-10
PRIOR APPLICATION NUMBER: 60/071,141
PRIOR APPLICATION NUMBER: 60/074,675
PRIOR FILING DATE: 1998-02-13
PRIOR FILING DATE: 1998-02-13
PRIOR FILING DATE: 1998-02-13
PRIOR FILING DATE: 1998-02-14
PRIOR FILING DATE: 1998-02-14
PRIOR FILING DATE: 1998-02-16
SOUTWARE: PatentIN Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 3; Length 123;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18.2%; Score 6; DB 3; Length 123; 100.0%; Pred. No. 63; tive 0; Mismatches C; Indels tive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 14
US-09-251-835-2
S-09-251-835-2
Patent No. 6261789
GENERAL INFORMATION:
APPLICANT: Reiter, Robert E.
APPLICANT: Witte, Owen N.
TITLE OF INVENTION: PSCA: PROSTAIE STEM CELL ANTIGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                           18.2%; Score 6; DB 3; 100.0%; Pred. No. 63; iive 0; Mismatches
PRIOR FILING DATE: 1998-61-12
PRIOR APPLICATION NUMBER: 60/674,675
PRIOR FILING DATE: 1998-02-13
PRIOR FILING DATE: 1998-03-10
NUMBER OF SEQ ID NOS: 16
SOFTWARE: PATENTIN VET: 2.0
SEQ ID NO 2
LENGTH: 123
                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: HUMAN PSCA (hPSCA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : ORGANISM: HUMAN PSCA (hPSCA)
US-09-203-939-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 100.
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6; Conservative
                                                                                                                                                                                                                                                                                                 ; LOCATION: (50)..(64)
; NAME/KEY: SITE
; LOCATION: (71)..(82)
; NAME/KEY: SITE
; LOCATION: (67)..(81)
US-09-203-939-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             111 PALGLE 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   111 PALGLE 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22 PALGLL 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22 PALGLL 27
                                                                                                                                                                                                                                                                                   NAME/KEY: SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 13
US-09-203-939-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                         FEATURE:
```

ô

ò

Search completed: September 26, 2003, 17:43:24 Job time: 6.89787 secs

us-09-852-100a-2_copy_185_217.rai

```
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compuger Ltd.
```

OM protein - protein search, using sw model

September 26, 2003, 17:41:48 : Search time 11.5149 Seconds (without alignments) 433.624 Million cell updates/sec Run on:

US-09-852-100A-2_COPY_185_217 33

1 VAVALSLFLGWLGADRFYLGYPALGLLKFCTVG 33 Perfect score: Sequence:

OLIGC Gapop 66.0 , Gapext 60.0 Scoring table:

566894 seqs, 151307093 residues Searched:

0 Word size

566894 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

(cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.prp: cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.prp: cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.prp: cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.prp: cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.prp: cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.prp: cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.prp: cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.prp: cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.prp: cgn2_6/ptodata/2/pubca/US08_PUBCOMB.prp: cgn /cgn2_5/ptodata/2/pubpaa/TS18C_PUBCOMB.pep:*/cgn2_5/ptodata/2/pubpaa/TS18C_NBW_TBR.pep:*/cgn2_5/ptodata/2/pubpaa/TS18C_WW_PB.pep:*/cgn2_5/ptodata/2/pubpaa/US8C_PUBCOMB.pep:*/cgn2_6/ptodata/2/pubpaa/US8C_PUBCOMB.pep:*/ Published_Applications_AA:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

			Description	Sequence 2, Appli	Sequence 2, Appl:	Sequence 2. App.	Sequence 288, App	Sequence 306, App	Sequence 28. Anni	Secuence 8, Apr.	Sequence 2. Appli	Sequence 27, Appl	Sequence 8, Appli	Sequence 6, Appli	Sequence 82, Appl	Sequence 82, Appl	Sequence 230, App	82,	
COLUMNATION			ID	US-09-852-100A-2	US-09-833-503A-2	US-10-199-881-2	US-1C-226-956-288								US-09-992-600A-82	US-09-924-340-82	US-09-974-879-230	US-09-992-095B-82	
			DB	. 6	10	15	15	25		0.7	::	11	15	10	1	11	11	12	
		Query	Length	269	569	269	21	21	24	27	27	27	27	221	221	221	221	221	
	oφo	Query	Match	100.0	100.0	100.0	24.2	24.2	24.2	24.2	24.2	24.2	24.2	24.2	24.2	24.2	24.2	24.2	
			Score	33	33	33	σ	œ	œ	œ	œ	80	œ	∞	æ	<b>3</b> 0	80	80	
		Result	S		7	m	4	'n	9	7	8	0	10	11	12	13	14	15	

185 VAVALSLFLGWLGADRFYLGYPALGLLKFCTVG 217

3

Sequence 82, App)	Sequence 82, App]	82,	82,	9	230	50,	48,	Sequence il, Appl	80,	CO	332,	332,	332,	332,	332,	332,	332,	332,		332,	332,	332,			7	332,	2,		332,
US-10 154-678-82	US-05-599-570-82	US-10-060-489-82	US-10-000-986-82	US-10-199-881-6	US-09-305-736-236	US-09-796-753-50	US-09-796-753-48	US-10-174-794-11	US-09-867-550-80	US-09-946-374-332	US-10-015-387A-332	US-10-006-130A-332	US-10-006-172A-332	US-10-015-392A-332	US-10-017-253A-332	US-10-017-306A-332	US-10-006-856A-332	US-10-006-818A-332	US-10-015-393A-332	US-10-015-869A-332	US-10-012-121A-332	US-10-006-116A-332	US-10-006-117A-332	US-10-017-527A-332	-10-01-	덖	-01	-10	US-10-012-755A-332
12	12	r)	15	12	11	11	17	12	5	11	12	12	12	12	12	12	15	15	15	15	15	15	15	15	15	15	15	15	12
221	221	221	221	221	222	230	247	358	122	173	173	173	173	173	173	173	173	173	173	173	173	173	173	173	173	173	173	173	173
24.2	24.2	24.2	24.2	24.2	24.2	24.2	24.2	24.2	21.2	21.2		21.2	٠	٠	٠	٠		•	21.2				•			•		21.2	21.2
3)	00	ග	ထ	ന	œ	œ	80	œ	7	7	7	7	7	7	7	7	7	٢	7	7	7	7	7	۲-	7	^	7	7	^
16	1.7	8.	19	20	21	22	23	24	25	26	2,	28	29	30	31	3.2	33	34	35	36	37	3.8	оћ (m)	<b>7</b>	41	4.2	43	4.4	۲. ۲.

### ALIGNMENTS

```
GENERAL INFORMATION:
APPLICANT: American Home Products
TITLE OF INVENTION: Beta-amyloid Peptide-Binding Proteins and Polynucleotices Enc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ..
C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 269;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9.4e-24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 VAVALSLFLGWLGADRFYLGYPALGLLKFCTVG 33
                                                                                                                                                                                                        LILE REFERENCE: AHP981251p2
CURREN: APPLICATION NUMBER: US/09/852,100A
CURREN: APPLICATION NUMBER: US/09/852,100A
CURREN: FILING DATE: 12001-05-09
PRICR APPLICATION NUMBER: US 09/172,990
PRICR PAPLICATION NUMBER: US 60/104,104
PRICR FILING DATE: 1998-10-13
PRICR APPLICATION NUMBER: PTC/US99/21621
PRICR APPLICATION NUMBER: US 09/060,609
PRICR APPLICATION NUMBER: US 60/064,583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 33; DB
100.0%; Pred. No. 9.4
tive 0; Mismatches
                                                     Sequence 2, Application US/09852100A Patent No. US20020058267A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cuery Match
Best Local Similarity 100.0
Matches 33; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Homo sapiens
RESULT 1
US-09-852-100A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-852-100A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8
```

```
APPLICANT: Bright, Gary R.
APPLICANT: Bright, Gary R.
APPLICANT: Bright, Gary R.
APPLICANT: Fremkumar, D. David
APPLICANT: Chen, Yih-Tai
TITLE OF INVENTION: NO. US20030104479Alel Fusion Proteins And Assays For Molecular
TITLE REFERENCE: 01-1022-US
CURRENT APPLICATION NUMBER: US/10/211,088
CURRENT APPLICATION NUMBER: 60/309,395
PRIOR APPLICATION NUMBER: 60/30915
PRIOR APPLICATION NUMBER: 60/3041,589
PRIOR FILING DATE: 2001-12-13
NUMBER OF SEQ ID NOS: 366
SOFTWARE: PatentIn Version 3.1
SEQ ID NO 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                 APPLICANT: JOSHI, LOKESH APPLICANT: JOSHI, LOKESH APPLICANT: JOSHI, LOKESH APPLICANT: SGAI, Brandon L.
TITLE OF INVENTION: REAGENTS AND METHODS FOR SMOOTH MUSCLE THERAPIES CURRENT APPLICATION NUMBER: US/10/226,956
CURRENT APPLICATION NUMBER: US/10/226,956
PRIOR APPLICATION NUMBER: 0/314,535
PRIOR FILING DATE: 2001-08-23
NUMBER OF SEQ ID NOS: 320
SEGTWARE: PATCHIN VORSION 3.1
SEGTWARE: PATCHIN VORSION 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CTHER INFORMATION: Protein-derived transport peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 24.2%; Score 8; DB 15; Best Local Similarity 100.0%; Pred. No. 0.5; Matches 8; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24.2%; Score 9; DB 15; 100.0%; Pred. No. 0.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               130.0%; Pred. h.v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                : CTHER INFORMATION: Synthetic peptide 35-10-226-956-288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : Sequence 28, Application US/09915914B : Publication No. US20030119725A1 : GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 305, Application US/10211089 Publication No. US20030164479A1 GENERAL INPORMATION:
                          Komalavilas, Padmini
                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
CRGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Divita, Gilles
APPLICANT: Fernandez, Joseph
APPLICANT: Heitz, Frederic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 130.0
Thes 8; Conservative
                                                    Panitch, Alyssa
APPLICANT: Brophy, Colleen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 LFLGWEGA 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7 LFLGWLGA 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 LFLGWLGA 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7 LFLGWLGA 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 5
US-10-211-088-306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-10-211-088-306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CS-09-915-914B-28
                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        S
                                                                                      GENERAL INCORDING.

APPLICANT: Ozonberger, Bradley A
APPLICANT: Ozonberger, Bradley A
APPLICANT: Ozonberger, Bradley A
APPLICANT: Carlos General Bradley A
APPLICANT: Lo, Ching-Hsiung F
APPLICANT: Lo, Ching-Hsiung F
APPLICANT: American Blome Products Corporation
TITLE OF INVENTION: No. US20020146760Aiel G-Protein-Coupled Receptor-Like Proteins an
TITLE OF INVENTION: Same
TITLE OF INVENTION: Same
TITLE OF INVENTION: Same
CURRENT APPLICATION NUMBER: US/69/833,503A
CURRENT FILING DATE: 2006-20-13
PRIOR APPLICATION NUMBER: 60/104,104
PRIOR APPLICATION NUMBER: 60/104,104
PRIOR FILING DATE: 1998-10-13
NUMBER OF SEG ID NOS: 6
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2. Application US/10199881

Publication No. US20030096356A1

GENERAL INFORMATION:
APPLICAMY: Wyeth
TITLE OF INVENTION: Encoded by Them, and Methods of Using Same"

ITILE OF INVENTION: Encoded by Them, and Methods of Using Same"

ITILE OF INVENTION: Encoded by Them, and Methods of Using Same"

ITILE OF INVENTION: Encoded by Them, and Methods of Using Same"

FILE REFERENCE: AHP9815651

CURRENT APPLICATION NUMBER: US/10/199,881

CURRENT FILING DATE: 1999-10-13

PRIOR FILING DATE: 1999-10-13

SOFTWARE: PATENTIN NUMBER: US 50/104,104

PRIOR FILING DATE: 1999-10-13

SOFTWARE: PATENTIN VETSION 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ŝ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gapsì
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ë
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 269;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ch 100.0%; Score 33; DB 15; Score 33; DB 15; Similarity 100.0%; Pred. No. 9.4e-24; 33; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 100.0%; Score 33; DB 10; Best Local Similarity 100.0%; Pred. No. 9.4e-24; Matches 33; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                185 VAVALSI,FLGWLGADRFYLGYPALGLI,FCTVG 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 VAVALSLFLGWLGADRFYLGYPALGI,LKFCTVG 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 VAVALSLFLGWLGADRFYLGYPALGLLKFCTVG 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 288, Application US/10226955
; Publication No. US20030060399Al
; GENERAL INFORMATION:
                                               Sequence 2, Application US/09833503A Patent No. US20020146760A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Homo sapiens
US-10-199-881-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
Matches 33; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-226-956-288
                       US-09-833-503A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-833-503A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 3
US-10-199-881-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 2
LENGTH: 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        a
```

```
APPLICANT: Wang, Rong-fu
ITILE OF INVENTION: Use of Celi-Penetraling Peptides to Generate Antitumor Immun:
FILE REFERENCE: P02373US1/10260806
CURRENT APPLICATION NUMBER: US/10/077,555
CURRENT FILING DATE: 2002-02-15
PRIOR APPLICATION NUMBER: US 60/258,687
PRIOR FILING DATE: 2001-02-15
NUMBER OF SEQ ID NOS: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Fernandez, Joseph
APPLICANT: Fernandez, Joseph
APPLICANT: Morris, Morris, Morris, Morris, Morris, Morris, Morris, May
APPLICANT: Mery, Jean
APPLICANT: Archdeacon, John
APPLICANT: Horndorp, Ky, e
11TLE OF INVENTION: PEPTIDE-MEDIATED DELIVERY OF MOLECULES INTO CELLS
FILE REFERENCE: AM-00105.P.1.1
CURRENT APPLICATION NUMBER: US/09/915,914B
CURRENT FILING DATE: 2001-07-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                               DB 11; Length 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 11: Length 27; . 0.63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24.2%; Score 8; DB 3
100.0%; Pred. No. 6.6
tive 0; Mismatches
                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                 Owery Match 24.2%; Score 5; I
Best Local Similarity 100.0%; Pred. No.
Matches 8; Conservative 0; Mismatch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: US 60/221,932
PRIOR FILING DATE: 2000-07-31
NUMBER OF SEQ ID NOS: 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: Synthetic sequence
                                                                                                                                           : OTHER INFORMATION: synthetic peptide
US-09-965-876A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 27, Application US/09915914B Publication No. US20030119725A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 8, Application US/10077555 Publication No. US20030077289A1 GENERAL INFORMATION:
                                                                                          TYPE: PRT
ORGANISM: ARTIFICIAL SEQUENCE
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin version 3.1
SEQ 1D NO 27
LENGTH: 27
                      SOFTWARE: Patentin version 3.1
SEQ ID NO 2
LENGTH: 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ouery Match
Hest Local Similarity 100.0
Free 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Divita, Gilles
    NUMBER OF SEQ ID NOS: 42
                                                                                                                                                                                                                                                                                                            7 LFLGWLGA 14
                                                                                                                                                                                                                                                                                                                                  7 LFLGWI,GA 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 LFLGWIGA 10
                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-915-914B-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JS-09-915-914B-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-077-555-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO 8
LENGIH: 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3
                                                                                                                                                                                                                                                                                                              ã
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Cellonics, Inc.
APPLICANT: Busa, William B
TITLE OF INVENTION: Methods and Reagents for Live-ceil Gene Expression Quantification
FILE REPERENCE: 00-789-A
CURRENT APPLICATION NUMBER: US/09/965,876A
CURRENT FILING DATE: 2001-09-28
PRIOR FILING DATE: 2000-09-28
PRIOR FILING DATE: 2000-09-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ġ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ξ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
GENERAL INFORMATION:
TAPLICATT C CTAIGN ROGET:
TITLE OF INVENTION: DELIVERY VEHICLES AND METHODS FOR USING THE SAME
FILE REFERENCE: 11067/2035
CURRENT APPLICATION UNMBER: US/09/785,802A
CURRENT APPLICATION NUMBER: US 09/748,05
PRIOR APPLICATION NUMBER: US 09/748,05
PRIOR PLING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
NUMBER OF SEC ID NOS: 16
SOGTWARE! PATENTION OF 16
SOGTWARE! 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Saps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                            APPLICANT: HOLIGOLD, Kyle
TITLE OF INVENTION: PEPTIDE-MEDIATED DELIVERY OF MCLECULES INTO CERTS
FILE PEPERENCE: AM-00105-p.13
CURRENT APPLICATION NUMBER: US/09/915,914B
CURRENT FILING DATE: 2001-07-26
PRIOR APPLICATION NUMBER: US 60/221,932
PRIOR FILING DATE: 2000-67-31
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PATENTIAN OF 13
LENGTH: 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0
                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 11; Length 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 27:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 8; DB 10;
Pred. No. 0.63;
                                                                                                                                                                                                                                                                                                                                                                                                                                      24.2%; Score 8; DB 1
100.0%; Pred. No. 0.5
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0: Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ) ORGANISM: Human immunodeficiency virus US-09-785-802A-8
                                                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: Synthetic sequence US-09-915-914B-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2, Application US/09965876A Publication No. US20030096243A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            : Sequence 8, Application US/09785802A
: Patent No. US20020151004A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24.2%; 3
                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Artificial Sequence
                        Mery, Jean
Archdeacon, John
                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 24.2
Best Local Similarity 100.
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
  Morris, May
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7 LFLGWLGA 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 LFLGWLGA 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
8; Conscreé
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILLILII
3 LFLGWLGA 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7 LFLGWLGA 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 8
US-09-965-876A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-785-802A-8
APPLICANT:
                                             APPLICANT:
                        APPLICANT
                                                                                                                                                                                                                                                                                                                                                    FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 7
```

a

ò

```
ö
                                                                                                                                                                                                                                                                 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                          MESON 11 13 13 4 340-82

Sequence 82, Application US/09924340

Publication No. US20030027248a1

SEQUENCE 82, Application US/09924340

SPECIANT: Bejanin, Stephane

APPLICANT: Bajanin, Stephane

APPLICANT: Tanaka, Hiroak

TITLE OF INVENTION: HUMAN CONSTELINS AND USES THEREOF

FILE REFERENCE: 91.US2.REG

CURRENT FILING DATE: 2001-08-06

PRIOR APPLICATION NUMBER: US 60/305,456

PRIOR FILING DATE: 2001-08-06

PRIOR APPLICATION NUMBER: US 60/302,277

PRIOR PELING DATE: 2001-06-29

SPRIOR PELING DATE: 2001-06-15

PRIOR PLING DATE: 2001-06-15

PRIOR PLING DATE: 2001-06-15

PRIOR APPLICATION NUMBER: US 60/293,574

PRIOR APPLICATION NUMBER: US 60/293,574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 221;
                                                                                                                                                                                                                  24.2%; Score 8; DB 11; Length 221;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                 indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 230, Application US/09974879
FUBLICATION NO. US20030028003A1
GENERAL INFORMATION:
APPLICAT: ROSEn et al.
ITLE OF INFUNITUR: 125 Human Secreted Proteins
FILE REFERENCE: P2020P2
CURRENT APPLICATION NUMBER: US/09/974,879
CURRENT FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: US 60/239,893
PRIOR FILING DATE: 2000-10-13
PRIOR FILING DATE: 2001-03-28
FRIOR FILING DATE: 2001-03-28
FRIOR FILING DATE: 2001-03-28
FRIOR FILING DATE: 105-2001-03-28
FRIOR FILING DATE: 105-2001-03-28
FRIOR FILING DATE: 105-2001-03-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                           Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 8; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24.2%; 5cc
106.0%; Pre
                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                         100.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ouery Match
Best Local Similarity luv...
8, Conservative
                                                                                                                                                                                                                  Query Match
Best Local Similarity 105.
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13 GADRFYLG 20
| | | | | | | | |
| 174 GADRFYLG 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Homo sapiens
                        LENGTH: 221
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                         13 GADREYLG 20
                                                                                                                    NAME/KEY: SIGNAL
LOCATION: 1..32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: SIGNAL
                                                                                                                                               US-09-992-600A-82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; LOCATION: 1.32
US-09-924-346-82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 14
US-09-974-879-230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQ ID NO 82
       SEQ ID NO 82
                                                                                                     FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ś
                                                                                                                                                                                                                                                                                                                                                             G
                                                                                                                                                                                                                                                                                                                                                                Sequence 6, Application US/09833503A

Patent No. US20020146760A1

GENERAL INFORMATION:
APPLICANT: Ozonberger, Bradley A

APPLICANT: Applicant Home Products Corporation
TITLE OF INVENTION: No. US20020146760A1el G-Protein-Coupled Receptor-Like Proteins an
TITLE OF INVENTION: Polynucleotides Encoded By Them, and Metrods of Using
TITLE OF INVENTION: Same
FILE REFRENCE: AHP58165-0CPCT
CURRENT APPLICANTION NUMBER: US/09/833,503A

CURRENT APPLICANTION NUMBER: US/09/104,104

PRIOR FILING DATE: 1998-10-13

NUMBER OF SEQ ID NOS: 6

SEGTWARE: PatentIN Ver. 2.1
                                                                                                                                                                      ċ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                      C: Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Tanaka, Hiroaki

TTLEOF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF

FILTE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF

FURENT APPLICATION: HUMAN CDNAS AND

CURRENT APPLICATION: HUMBER: US/09/992,600A

CURRENT APPLICATION NUMBER: US/09/992,600A

PRIOR PILING DATE: 2001-08-06

PRIOR PILING DATE: 2001-08-06

PRIOR PILING DATE: 2001-08-06

PRIOR APPLICATION NUMBER: US 60/294,696

PRIOR PILING DATE: 2001-06-29

PRIOR PILING DATE: 2001-06-29

PRIOR PILING DATE: 2001-06-29

PRIOR APPLICATION NUMBER: US 60/294,696

PRIOR PILING DATE: 2001-06-15

PRIOR PILING DATE: 2001-06-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .;
O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 10; Length 221;
                                                                                                                         Length 27;
                                                                                                                                                                   0: indels
                                                                                                                         DB 15;
                                                                                                                  Query Match 24.2%; Score 8; DH 1
Best Local Similarity 100.0%; Pred. No. 0.5
Matches 8; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24.2%; Score 8; DB 1
100.0%; Pred. No. 4;
ive 0: Mismatches
                                                 CTHER INFORMATION: Synthetic Poptide US-10-077-555-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 82, Application US/09992600A Publication No. US20030027161A1 GENERAL INFORMATION: APPLICANT: Benjanin, Stephane
ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 160.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 114
SOFTWARE: JPatent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
CORGANISM: Homo sapiens
US-09-833-503A-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 174 GADRFYLG 181
                                                                                                                                                                                                                  7 LFLGWLGA 14
                                                                                                                                                                                                                                              3 LFLGWLGA 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13 GADRFYLG 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 12
US-09-992-600A-82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
```

0; Gaps

Sength 221; 0; Indels

```
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Search completed: September 26, 2003, 17:55:13 Job time: 12.5149 secs
                                                                                                                                                                                                                                                                                                                                                        Score 8; i
Pred. No.
                                                                                                                                                                                                                                                                                                                                     24.2%; 5c.
100.0%; Pre
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 112
SOFWARE: 3Patent
SEQ ID NO 82
LENGTH: 221
                                                                                                                                                                                                                                                                                                                                                     Ouery Match
Bost Local Similarity 100.
Matches 8; Conservative
                                                                                                                                                      TYPE: PRI
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13 GADRFYLG 20
                                                                                                                                                                                                                                   ; NAME/KEY: SIGNAL
; LOCATION: 1..32
US-09-992-0958-82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION: (184)
COTHER INFORMATION: Xee equals any of the naturally occurring tramine acids US-09-974-879-230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 82, Application US/0992095B

Publication No. US20030157485A1

GENERAL INFORMATION:

APPLICANT: Benjanin, Stephane
APPLICANT: Tanaka, Hiroaki

TILE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF
FILE REFERENCE: 91.US5.DIV
CURRENT FILING DATE: 2003-02-20

PRIOR PRIOR APPLICATION NUMBER: US 09/924,34C

PRIOR FILING DATE: 2001-08-06

PRIOR FILING DATE: 2001-08-06

PRIOR PRIOR OFFICATION NUMBER: US 60/305,456

PRIOR PRIOR APPLICATION NUMBER: US 60/305,456

PRIOR FILING DATE: 2001-07-13

PRIOR PLING DATE: 2001-07-13

PRIOR PLING DATE: 2001-07-13

PRIOR PLING DATE: 2001-06-05

PRIOR PLING DATE: 2001-06-05

PRIOR PLING DATE: 2001-06-05

PRIOR PRING APPLICATION NUMBER: US 60/302,277

PRIOR PRING DATE: 2001-06-15

PRIOR PLING DATE: 2001-06-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24.2%; Score 8; D3 11; Rength 221; 100.0%; Pred. No. 4; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                        PRIOR FILING DATE: 1998-11-34
PRIOR APPLICATION NUMBER: US 60/064,911
PRIOR FILING DATE: 1997-11-07
PRIOR FILING DATE: 1997-11-07
PRIOR FILING DATE: 1997-11-07
PRIOR APPLICATION NUMBER: US 60/064,983
PRIOR APPLICATION NUMBER: US 60/064,900
PRIOR APPLICATION NUMBER: US 60/064,900
PRIOR FILING DATE: 1997-11-07
PRIOR PRIOR APPLICATION NUMBER: US 60/064,987
PRIOR FILING DATE: 1997-11-07
PRIOR PAPLICATION NUMBER: US 60/064,987
PRIOR PLICATION NUMBER: US 60/064,987
PRIOR PELING DATE: 1997-11-07
PRIOR FILING DATE: 1997-11-17
      PRIOR APPLICATION NUMBER: PCT/US98/23435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 60/293,574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 24.2
Best Local Similarity 100.
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13 GADRFYIG 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 15
US-09-992-095B-82
```

```
GenCore version 5.1.6
Copyright (c) 1993 - 2063 Compugen Ltd.
```

OM protein - protein search, using sw model

September 26, 2003, 17:28:28 ; Search time 3.93192 Seconds (without alignments) 394.688 Million cell updates/sec Run on:

US-09-852-100A-2_COPY_185_217 33 1 VAVALSLFLGWLGADRFYLGYPALGLIKFCTVG 33 Title: Perfect score: Sequence:

OLIGO Gapop 60.0 , Gapext 60.0 Scoring table:

127863 seqs, 47026705 residues Searched:

0

Word size :

Total number of hits satisfying chosen parameters:

127863

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

SwissProt_41:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

pt. ion	omo sapi bollos sapi bollos sapi bollos sapi bollos sapi scherich scherich scherich scherich scherich scherich scherich scherich scherich scherich scherich scherich scherich scherich scherich scherich scherich scherich scherich scherich scherich scherich scherich scherich scherich scherich scherich scherich scherich scherich scherich scherich scherich scherich scherich scherich scherich scherich scherich scherich scherich scherich scherich scherich scherich scherich scherich scherich scherich scherich scherich scherich scherich scherich scherich scherich scherich scherich scherich scherich scherich scherich scherich scherich scherich scherich scherich scherich scherich scherich scherich scherich scherich scherich scherich scherich scherich scherich scherich scherich scherich scherich scherich scherich scherich scherich scherich scherich scherich scherich scherich scherich scherich scherich scherich scherich scherich scherich scherich scherich scherich scherich scherich scherich scherich scherich scherich scherich scherich scherich scherich scherich scherich scherich scherich scherich scherich scherich scherich scherich scherich scherich scherich scherich scherich scherich scherich scherich scherich scherich scherich scherich scherich scherich scherich scherich scherich scherich scherich scherich scherich scherich scherich scherich scherich scherich scherich scherich scherich scherich scherich scherich scherich scherich scherich scherich scherich scherich scherich scherich scherich scherich scherich scherich scherich scherich scherich scherich scherich scherich scherich scherich scherich scherich scherich scherich scherich scherich scherich scherich scherich scherich scherich scherich scherich scherich scherich scherich scherich scherich scherich scherich scherich scherich scherich scherich scherich scherich sche	D 18100
SUMMARIES 15	KKTA_HUMAN YPUC_BACSU CUCH_HUMAN CYB_RHOW1 CG551_HUMAN CYB_ECCULI ITRI_SCHPO LITRI_SCHPO LITRI_SCHPO LITRI_SCHPO LITRI_SCHPO LITRI_SCHPO LITRI_SCHPO LITRI_SCHPO LITRI_SCHPO TY13_HUMAN GTH2_MOREA PSAG_RATH PSAG_RATH PSAG_RATH PSAG_RATH CTHP_MOREA PSAG_RATH CHOULVIBCH TABP_ITHECE TAB	ב כ
ch DB	222000 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	1
		i
Score		>
		)

6 18.2 254 : SURE_YERPE	ALIGNMENTS STANDAND; PKT; 358 AA. pl. 25, Created) pl. 25, Last sequence update)	16-5CT-2001 (Rel. 40, Jast annotation update) Scrine/threonine-protein kinase KKIALRE (EC 2.7.1) (Cyclin-dependent Kinase-like 1). COKLI. Homo sapiens (Human). Eukaryota: Metazoa; Chordata: Craniata; Vertebrata: Euteleostomi; Mammalia: Eutheria; Primates; Catarrhini; Hominidae: Homo.	JUENCE FROM N.A. LINES-93437325; Pubmed-1639063; PLINES-93437325; Pubmed-1639063; Person M., Enders G.H., Wu CL., Sw. LK., Gorka C., Nelson C., Ilow E., Tsai LH.: If mily of human cdc2-related protein kinases."; Go. J. 11:2909-2917(1992). SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES. CDC2/CDKX SUBFAMILY.	SEMISS-PROT entry is copyright. It is produced through a collaboration seen the Swiss Institute of Bioinformatics and the EMBL outstation European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way lifted and this statement is not removed. Usage by and for commercial titles requires a license agreement (See http://www.isb-sib.ch/announce/send an email to license@isb-sib.ch).	3L; X66358; CAA47002.1: 3L; X66359; CAA47002.1; JOINED. 3L; X66359; CAA47002.1; JOINED. 3R; S23483; S23383.3 5P; P24941; HCL. 3C00523 5C05341; JHCL.	CO; GO:0004693; F:cyc.in-dependent protein kinase activity; TAS. CO: GO:0004648; P:protein amino acid phosphory.ation: TAS. CO: GO:0000074; P:protein amino acid phosphory.ation: TAS. CO: GO:0000074; P:requiation of cell cycle; TAS. InterPro: IPR000719; Prot_kinase. InterPro: IPR002290; Ser thr_pkinase. Pfam; PF00069; pkinase, I. Probom; PD000001; Prot_kinase, I. SMART; SM00220; S_TKc; I. PROSITE; PS00107; PROTEIN_KINASE_ATP; I.	OSITE; PSSOUL; PROTEIN_KINNSE_DOM; 1.  ansferase; Serine/threonine-protein kinase; ATP-binding.  5 288 PROTEIN KINASE.  BIND 11 19 ATP (BY SIMILARITY).  NDING 34 34 ATP (BY SIMILARITY).  "SITE 127 127 BY SIMILARITY.  "SITE 127 127 BY SIMILARITY.  "UENCE 358 AA; 41834 MM; 88344321F24877C6 CRC64;
መስመመስመቋቋቋቋቋ ቀመማኮመውዕጋዛልሠቋቋ	2, ₹	DE SET 15- DE KID SET 00 COS HOME COS HOME COS HOME COS NAME COS N	SEO	cc use the	DX EMB DX EMB DX EXS DX ESS DX GX	DR GO: DR GO: DR Interpretation of Pro- DR Pro- DR PRO- DR PRO- DR PRO- DR PRO-	KW Tra

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the FMEL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RA KUDLINE-980440403; Jubmed-235437;

RA KUDLINE-980440403; Jubmed-235437;

RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Rorchert S., Bartisher L., Brans A., Braun M., Brigarell S.C., Bron S., Brouillet S., Bourshier L., Brans A., Braun M., Brigarell S.C., Bron S., Brouillet S., Bourshier L., D., Connerton I.F., Cummings N.J., Daniel R.A., Deniel R.M., Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A., Deniel R.M., Dusterhoff A., Errichich S.D., Emmersson P.I., Ranian K.D., Errington J., Fabret C., Ferrari E., Follger D., Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galieron N., Guiseppi G., Guy B.J., Haga K., Halech J., Harwood C.R., Henaut A., Hibbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L., Andrian D., Kasahara Y., Klaerr Elunchard M., Klein C., Koetter P., Koningstein G., Krodh S., Kumano M., Kurita K., Levine A., Luu H., Masuda S., Mauel C., Medgue C., Rohadshi Y., Koningstein G., Radeina N., Mellado R.P., Miruno G., Krodh S., Kumano M., Mesin D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H., Rafer D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H., Rafer D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Resoch E., Pujic P., Purnelle B., Ropeoport G., Roye M., Reynolds S., Schroeter R., Scanlan E., Schroeter R., Yasamott R., Wedler E., Yoshikawa H., Zanstein Bacilius R., Nohn Wenner M., Wenner M., Wenner M., Wenner M., Wenner M., Wenner 
                                                ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Sequence analysis of the Bacilius subtilis chromosome region between
the serA and kdg loci cloned in a yeast artificial chromosome.";
Microbiology 142:2005-2016(1996).
                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sorokin A.V., Azevedo V., Zumstein E., Galleron N., Ehrlich S.C..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
                                                   .
O
Length 358;
                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Firmicutes; Bacillales; Bacillaceme; Bacil.us.
     DB 1;
                                                                                                                                                                                                                                                                                                               01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Hypothetical protein ypjC.
24.2%; Score 8; DB 1
100.0%; Pred. No. 1;
iive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=168;
MEDLINE=98644033; PubMed=9384377;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-168 / Marburg;
MEDLINE-96349105; Pubmed*8760912;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nature 390:249-256(1997).
                         Best Local Similarity 100.
Matches 8; Conservative
                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                259 YPALGLLK 266
                                                                                                 21 YPALGILK 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                               YPJC OR JOJC.
Bacillus subtilis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=1423;
                                                                                                                                                                                                                                                                      YPJC_BACSU
P42978;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Serror P.;
     Query Match
                                                                                                                                                                                                                                                  YPUC_BACSU
```

```
MEDLINE-20289799; Pubbed=10830953;
A Hattori M., Fujiyama A., Taylor T.D., Watanabe H., Yada J.,
A Fuzix H.-S., Toyoda A., Ishli K., Totoki Y., Chol D.-K., Groner Y.,
A Soeda E., Ohki M., Takagi T., Sakaki Y., Taudien S., Blechschmidt K.,
Polley A., Henzel U., Delabar J., Kumpf K., Lebmann R., Patterson D.,
Reichwald K., Rump A., Schillhabel M., Schudy A., Zimmermann W.,
A Rosenthal A., Kudoh J., Shibuya K., Mawasaki K., Asakawa S.,
A Shintani A., Sasaki T., Nagamine K., Mitsyama S., Antonarakis S.B.,
Minoshima S., Shimizu N., Nordsiek G., Hornischer K., Brandt P.,
A Raser J., Beck A., Klages S., Hennig S., Riesselmann L., Dagand E.,
Merimeyer S., Borzym K., Gardiner K., Nizetic D., Francis F.,
Lehrach H., Reinhardt R., Yaspo M.-L.;
The DNA sequence of human chromosome 21.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL. Outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
Usage by and for commercial
                       entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          О
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata: Craniata; Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates; Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1; Length 215;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             D; Indeis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
Keen T.J., Inglehearn C.F.:
Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -:- FUNCTION: COMPONENT OF TIGHT JUNCTION (TJ) STRANDS.-:- SUBCELLULAR LOCATION: Integral membrane protein.-:- SIMILARITY: Belongs to the claudin family.
                                                                                                                                                                                                                                           Fire very months; BG11209; ypjG.
InterPro; IPR05740; DUF161.
IRANSMEM 31.
FIRENSMEM 51.
FIRENSMEM 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                104 124 POTENTIAL.
215 AA; 23582 MW; D314CF7225F8A983 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30-MAY 2000 (Rel. 39, Created)
30-MAY 2000 (Rel. 39, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21.2%; Score 7; DB 1
100.0%; Pred. No. 7;
Live 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL.
                                                                                                                       EMBL, L38424, AAA92872.1; -. EMBL, L47709, AAB38440.1; -. EMBL. 259115; CAB14167.1; -. PITR, C69937. C69937.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nature 405:311-319(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13 VALSLFL 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 VALSLFL 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CEDH_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claudin-17.
CLDNJ7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    TRANSMEM
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                     TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CIDHLHUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     a
ô
```

EMBL; AJ250712; CAB60616.1; -

 $\sim$ 

```
8 FLGWLGA 14
                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                               NCBI_TaxID=9606
                                                                                                                                                                                                                                                                                                        TISSUE=Embryo;
                                                                                     _HCMAN
                                                                                                                                                                                     έ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            respiratory chain that generates an electrochemical potential. Coupled to ATP synthesis (By Similarity).

COFACTOR: Binds two heme groups non-covalently, Heme 1 (or Bi. or b562) is low-potential and absorbs at about 552, and heme 2 (or EH or b566) is high-potential and absorbs at about 566 (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                             Verbist J., Lang F., Gabellini N., Oesterhell D.; "Cloning and sequencing of the fbc?, B and C genes encoding the cytochrome D/C | complex from Rhodopseudomonas vizidis."; Mol. Gen. Genet. 219:445-452(1989).

Mol. Gen. Genet. Component of the ubiquinol-cytochrome c reductase complex (complex III or cytochrome b-ci complex), which is a
                                                                                                                                                                                     ó
                                                                                                                                                                                                                                                                                                                                                          Rhodopseudomonas viridis.
Bacteria; Proteobacteria; Alphaprotecbacteria; Rhizobiales;
                                                                                                                                                                Length 224;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1; Length 419;
                                                                                                                                                                                     0; Indels
                                                                                                                                          1833ED3178B7F63A CRC64;
                                                                                                                                                               DB 1;
                                                                                                                                                                                                                                                                                                    15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                   419 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21.2%; Score 7; DB 1
100.0%; Pred. No. 11:
tive 0; Mismatches
                                                                                                                                                                                   0; Mismatches
                                                                                                                                                              Score 7; Di
Pred. No.
                                                                                                POTENTIAL
                                                                                                                      POTENTIAL
                                                                                                           POTENTIAL
                                                                                                                                POTENTIAL
          Genew, HGNC:2038; CLDN17:
InterPro: IPR006187; Claudin.
InterPro: IPR006189; Claudin.sup.
InterPro: IPR004031; PMF22_Claudin.
Pfan: PP00822; PMP32_Claudin.
PRINTS; PR01077; CLAUDIN: I.
                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-90158506; PubMed-2560136;
                                                                                                                                                                                                                                                                                                                                                                             Hyphomicrobiaceae; Blastochloris.
NCBI_TaxID=1079;
EMBL; AP001707; BAA95566.1; ..
                                                                                    Tight junction; Transmembrane.
TRANSMEM 8 28 P
TRANSMEM 82 102 P
                                                                                                                                          24603 MW;
                                                                                                                                                              21.2%;
                                                                                                                                                    Query Match
Best Local Similarity 100...
7; Conservative
                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                    145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
7; Conserve
                                                                                                                   125
165
165
224 AA;
                                                                                                                                                                                                                              86 VAVALSL 92
                                                                                                                                                                                                        1 VAVALSL 7
                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                     Cytochrome b.
                                                                                                                                                                                                                                                                                                                                                 PETS OR FBCB
                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=DSM
                                                                                                                                                                                                                                                                                 CYB_RHOVI
P81378;
                                                                                                                      TRANSMEM
                                                                                                                                TRANSMEM
                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                             RESULT 4
CYB_RHOVI
 ã
```

Gaps

.; 0

0; Indels

Conservative

```
MEDININE-2003/105 Pubbmed-10591208

MEDININE-2003/105 Pubbmed-10591208

Dunham I., Hunt A.R., COllins J.E., Bluckiewich R., Beare D.M., Clamp M., Smink I.J., Ainscough R., Almeida J.P., Babbage A.K., Barder C., Barder S.M., Buckers S.M., Collins B. Barder C., Carter N.P., Chen Y., Clark G., Barder C., Carter N.P., Chen Y., Clark G., Carder C., Collier R.E., Conner R., Conrey D., Cortry N.R., Coville G.J., Cox A.V., Davis J., Duwson E., Chami P.D., Dockree C., Dodsworth S.J., Durbin R.M., Ellington A.G., Shami P.D., Dockree C., Dodsworth S.J., Durbin R.M., Ellington A.G., Shami P.D., Dockree C., Dodsworth S.J., Durbin R.M., Ellington A.G., Shami P.D., Dockree C., Dodsworth S.J., Durbin R.M., Ellington A.G., Shall R.E., Hall Tranlyn G., Heathcott R.W., Ho S., Holmes S., Holmes S., Hall R.E., Jones M.C., Fershaw J.Y., Kimberloy A.M., King M.M., Lioyd C., Lloyd D.M., Antyn I.D., Mashreghi Hohammadi M., Matthews L.H., Mccann O.T., Andelin S.J., Mclaren S., Mcwurray A.A., Milne S.A., Mortimore B.J.C.T., R. Antyn I.D., Mashreghi Hohammadi M., Mallis S.H., Mortimore B.J.C.T., R. Andelin S.J., Mclaren S., Mcwurray A.A., Milne S.A., Mortimore B.J.C.T., Soderlund C., Spragon L., Steward C.A., Sdiston J.E., Swann R.M., Stude C.L., Spragon L., Steward C.A., Sdiston J.E., Swann R.M., Williams S.H., Williams S.A., Williamson H., Willey D.R., Shinizu N., Williams S.A., Williams S.A., Williams S.A., Williamson H., Williams S.A., Williams S.A., Williamson H., Williams S.A., Chen F., Chu L., Crabtree J., Deschamps S., Do A., Do T., R. Mincahi A., Shiniza M., Rang K., Hu P., Hu P., Hu P., Hu P., Willer H., Yao Z., Lewis S., Linn S.-P., Loh P., Manj Y., Manj K., Manj K., Manj G., Willer N., Miller N., Manj G., Chissoe S., Murray J., Miller N., Mins P., Danson D., Bentley D., Graves T., Hawkins J., Lewis S., Lulton L., Goela D., Graves T., Hawkins J., Bardshaw H., Bourne S., Corder S., Changer S., Harley D., Graves T., Hawkins J., Lewis S., Lilton L., Goela D., Graves T., Hawkins J., Hawkins J., Lewis S., Lilton L., Goela D., Graves
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Isogai T., Ota I., Hayashi K., Sugiyama I., Otsuki T., Suzuki Y., Nisikawa T., Nagai K., Sugano S., Shiratori A., Sudo H., Sudo H., Wagatsuma M., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M., Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S., Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K., Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y., Ninomiya K., Iwayanagi T., Nakamura Y., Nagahari K., Masuho Y., Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human).
Sukaryota: Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia: Eutheria: Primates; Catarrhini; Hominidae: Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A., AND VARIANT ILF-345.
MEDLINE-20272150; Pubmed-10810093;
Tai C.-H., Chou C.-Y., Ch'ang L.-Y., Liu C.-S., Lin W.-C.;
"Identification of novel human genes evolutionarily conserved in Caenorhabditis eigens by comparative proteomics.";
Genome Res. 10:703-713(2000).
                                                                                                                                                             097512; 096999; 096146; 090W85; 0900W9; 16-0CT-2001 (Rel. 40, Created) 28-FEB-2003 (Rel. 41, Last sequence update) 15-SEP-2003 (Rel. 42, Last annotation update) CG1-51.
                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE=20057165; PubMed-10591208;
                                                                                                                                               STANDARD;
```

Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales, Enterobacteriaceae, Escherichia

Plasmid ColBM-pF166

NCBI_TaxID=562;

Escherichia coli

C1-NOV-1988 (Rel. 09, Created) C1-JUL-1989 (Rel. 11, Last sequence update) 28-FEB-2003 (Rel. 41, Last annotation update) Colicin B.

```
8 TTTTTWW RRANGES READ BEST RESERVED BEST RE
                                                                                                                                                                                                                                                                                                                                      RA STRUENCE FROM NA.

RA STRUEPLYMPh, MUSCLE and Skin,

RA STRUEPCR R.L., Feingold E.A., Grouse L.M., Derge J.G.,

RA Altschul S.P., Zeeberg R.L., Fringold E.A., Grouse L.M., Schaefer C.F., Bhal N.K.,

RA Altschul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bhal N.K.,

RA Altschul S.P., Jordan H., Moore T., Max S.I., Wang C., Haler F.,

RA Altschul S.P., Jordan H., Moore T., Max S.I., Wang C., Haler F.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carnicol P., Prange C.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carnicol P., Prange C.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carnicol P., Prange C.,

RA Brownstein M.J., Worley K.C., Hale S., Garcian P.H.,

RA Richards S.A., McEvan P.J., McKernan K.J., Malek J.A., Scheetz T.E.,

RA Richards S.A., McEvan P.J., McKernan K.J., Malek J.A., Sibbs R.A.,

RA Nillalon D.K., Muzny D.M., Soderqren E.J., LN X., Sibbs R.A.,

RA Willalon D.K., Muzny D.M., Soderqren E.J., LN X., Sibbs R.A.,

RA Niting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Ra Butterfield Y.S.N. Krzywinski M.I., Skalska J., Smailus D.E.,

RA Schnerch A., Schein J.E., Jones S.J. M., Marra M.A.,

Rand mouse cDNA sequences.",

RT Human and mouse cDNA sequences.",

RT Proc. Natl. Acad. Scil. U.S.A. 99:16903:2502).

C. --- SIMILARITY: BELONGS TO THE UPP0140 (CGI-51) FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright, it is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its wore by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                      Scheet P., Walker C., Wamsley A., Wohldmann P., Pepin K., Neison K., Korf I., Bedell J.A., Hillier L., Mardis E., Waterston R., Wilson R., Emanuel B.S., Shaikh T., Kurahashi H., Saitta S., Budarf M.E., McDermid H.E., Johnson A., Wong A.C.C., Morrow B.E., Edelmann L., Seroussi E., Fransson I., Tapia I., Bruder C.E., O'Brien K.P., Wilkinson P., Bodenteich A., Hartman K., Hu X., Khan A.S., Lane L., Tilahun Y., Wright H.; The DNA Sequence of human chromosome 22.7;
Hinds K., Kemp K., Latreille P., Layman D., Ozersky P., Rohlfing T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         110 110 b -> G (IN REF. 2).
368 372 WAGGL -> JGREW (IN REF. 1).
371 MISSING (IN REF. 4; AAH07830).
469 AA; 51962 MW; 4F687D27A12092EF CHC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1; Length 469; . 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         V -> I (IN dbSNP:8418).
/FIId*VAR_013768.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; BC015200; AAH15200.1; -.
InterPro; IPR000184; Bac_surfAg_D15.
Pfam; PF01103; Bac_surface_Ag: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21.2%; Scur
160.0%; Pre
0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL, AK001087; BAA91498.1; --
EMBL, AF151809; AAD34046.1; --
EMBL, AL035398; CAB51401.1; --
EMBL, BC007930; AAH07836.1; --
EMBL, BC011681; AAH1681.1; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
nes 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Polymorphism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Loc
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL curstation the Furopean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ó:
SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.

X MEDLINE-87250309; Pubmed-249491;
Schramm E., Mende J., Braun V., Kamp X.M.;
Schramm E., Mende J., Braun V., Kamp X.M.;
Schramm E., Mende J., Braun V., Kamp X.M.;

Nucleotide sequence of the colicin B activity gene cba: consensus

T pertapeptide among Tona-dependent colicins and receptors.";
J. Bacteriol. 169:3350-3357(1987).

-:- FUNCTION: THIS COLICIN IS A CHANNEL-FORMING COLICIN. THIS CLASS OF

TRANSMEMBRANE TOXINS DEPOLARIZE THE CYTOPLASMIC MEMBRANE, LEADING

C:- FUNCTION: COLICINS ARE POLYPEPTIDE TOXINS PRODUCED BY AND ACTIVE

AGAINST, ESCHERICHIA COLI AND CLOSELY RELATED BACIERIA.

-:- MISCELLANBOUS: THIS COLICIN REQUIRES TONB FOR ITS UPTAKE.

-:- SIMLARITY: HIGH IN THE N-TERMINAL FIRST 300 AMINO ACID RESIDUES

-:- HITH COLICIN D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                      -!- SIMILARITY: WITH OTHER CHANNEL FORMING COLICINS, HIGHEST WITH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRINTS; PRO0280; CHANLCOLICIN.
PRINTS; PR01295; CLOACIN.
PRODOM; PR002657; CABANGAL-Colicin: 1.
PROSITE: PS00275; CHANNEL_COLICIN: 1.
PROSITE: PS00430; TONE_DEPENDENT_REC_1: 1.
Antibictic: Bacteriocin: Plasmid; Transmembrane; Tonb box.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 510;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6E4B972CF19245F1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ITRI_SCHPO STANDARD: PRT; 575 AA 010286; 01.NOV-1997 (Rel. 35, Last sequence update) 01.NOV-1997 (Rel. 35, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.08; Pred. ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POTENTIAL.
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Interpro; IPR005293; Channel_colicin.
InterPro; IPR003088; Cloacin.
InterPro; IPR003081; TonB_boxC.
Pfam; PP03515; Cloacin; 1.
Pfam; PF01024; Colicin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TONB BOX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    54732 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; M16816; AAA98063.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21.28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ouery Match
Dest Local Similarity luv...
Loc 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PIR; A27089: IKECBB.
HSSP; P04480; ICOL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            454 4
476 4
510 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 457 AVALSLF 463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 AVALSLF 8
                                                                                                                                                                                                                                                                                                                                                                                                       COLICIN A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TRANSMEM
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ITR1_SCHPC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AC
DE
```

ö

Gaps

0

0; indels

Mismatches

Conservative

510 AA.

PRT;

STANDARD;

CEAB_ECOLI ID CEAB_ECOLI

RESULT 6

```
RESULT 8
LIK2_RAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ô
                                                                                                                                                                                                                                                                                                                                           RECORD NO. CONTINUED FOR THE STATE OF THE ST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROI entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                        Niederberger C., Graub R., Schweingruber A.-M., Faukhauser H., Rusu M., Poitelea M., Edenharter L., Schweingruber M.E.;

"Exogenous inositol and genes responsible for inositol transport are required for mating and sporulation in Shizosaccharomyces pombe.";
Curr. Genet. 33:255-261(1998).
              Myo-inositol transporter 1.
ITRI OR SPACTP4.G1.
Schizosaccharomyces pombe (Fission yeast).
Eukaryota, Fungl; Ascomycota: Schizosaccharomycetes:
Schizosaccharomycetales; Schizosaccharomycetes:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS00216; SUGAR_TRANSPORT_1; 2.
PROSITE; PS00217; SUGAR_TRANSPORT_2; FALSE_NEG.
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GeneDB_SPOMDe; SPAC4F8.15; -.
InterPro; IPR007114; MFS.
InterPro; IPR005828; Sub_transporter.
InterPro; IPR005829; Sug_transporter.
InterPro; IPR00363; Sugar_transpt.
Pfam; PF00083; Sugar_tr; 1.
PRINTS; PR00171; SUGRTRNSPORT.
                                                                                                                                                                                           MEDLINE=98228265; PubMed-9560432;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL, X98622, CAA67211.1; -. EMBL, 298530, CAB11061.1; -. EMBL, 299532, CAB16718.1; -. PIR; T43400, T43400.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TIGR00879; SP; 1.
                                                                                                       Schizosaccharomyces
                                                                                                                                            [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                           NCBI_TaxID-4896
                                                                                                                                                                             STRAIN-968 h90
                                                                                                                                                                                                                                                                                                                                      STRAIN-972
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FIGRFAMS;
```

```
Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euleleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FUNCTION: DISPLAYS SERINE/THREONINE-SPECIFIC PHOSPHORYLATION OF MYELIN BASIC PROTEIN AND HISTONE (MBP) IN VITRO (BY SIMILARITY). SUBCELLULAR LOCATION: Cytoplasmic (By similarity). ALTERNATIVE PRODUCTS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Isold-P53670-4; Sequence-VSP_003128, VSP_C03131;
-:- TISSUE SPECIFICITY: FOUND IN VARIOUS TISSUES AT MODERATE LEVELS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=Wistar; TISSGE-Brain:
BEDLINE=25380177; Pubmed=7651734;
Nunoue K., Ohashi K., Okano I., Mizuro K.;
"LIMK-1 and LIMK-2, two members of a LIM motif-containing protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  isoId=P53670-3; Sequence=VSP_003128, VSP_003129, VSP_003130;
                                                                                                                                                                                                                                                                                                                                                                                                                   (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (ISOFORMS LIMK2A; LIMK2B; LIMK2C AND LIMK2D)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1; Length 575;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                    EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                        EXTRACELLULAR (POTENTIAL).
8 (POTENTIAL).
                                                                                                             EXTRACELLULAR (POTENTIAL)
                                                                                                                                                         5 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                    EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                            3B7C5EFF86C596AE CRC64;
                                               EXTRACELLULAR (PCTENTIAL)
                                                                                                                                                                                                        CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                        CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                       CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                  CYTOPLASMIC (POTENTIAL).
N-LINKED (GLCNAC. . .) (
                  CYTOPLASMIC (POTENTIAL).
                                                                             CYTOPLASMIC (POTENTIAL)
                                                                                                                                           CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Event=Alternative splicing; Named isoforms=4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-0cf-1996 (Rel. 34, Created)
C1-0cT-1996 (Rel. 34, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                       (POTENTIAL).
                                                                                                                                                                                                                                                                                                                   (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                       (POTENTIAL)
                                                                                                                                                                                                                          7 (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                          (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28-FEB-2003 (Rel. 41, Last annotation upda
LIM domain kinase 2 (EC 2.7.1.-) (LIMK-2).
                                                                                                                            4 (POTENTIAL)
                                                                                                                                                                                                                                                                                        (POTENTIAL)
                                                                                            3 (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IsoId=P53670-2; Sequence=VSP_003128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IsoId-P53670-1; Sequence-Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 7;
Transmembrane; Sugar transport;
                                                                                                                                                                                                                                                                                                                                                                                                                                  62757 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21.28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    kinase family.";
Oncogene 11:701-710(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cucry Match
Best Local Similarity 100...
7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                              107
128
128
127
127
207
                                                                                                                                                         2336
2245
2267
3346
3346
3346
3346
562
562
563
573
575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 511
532
432
575 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8 FLGWLGA 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Name-LIMK2B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Name-LIMK2C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Name-LIMK2D;
                                                                                                                                                                                                        268
3371
377
377
398
442
442
463
463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Name-LIMK2A
                                                                                                                                                                                                                                                                                                                                                                  208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LIK2_RAT
P53670;
                                                DOMAIN
                                                                               DOMAIN
TRANSMEM
                                                                                                                                           DOMAIN
                                                                                                                                                                           DOMAIN
TRANSMEM
                                                                                                                                                                                                                                           DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
CARBOHYD
                                                                                                                                                                                                                                                                                                                       TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                       TRANSMEM
                               RANSMEM.
                                                                                                                          FRANSKEM
                                                                                                                                                                                                                          TRANSMEM
                                                                                                                                                                                                                                                                                       TRANSMEM
                                                                                                                                                                                                                                                                                                                                                       TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LIMK2.
```

ö

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation. The European Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SWEGGSCDSCSHR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BY SIMILAKITY.
MARAGGERAMRORGGNYVPLSGRLYRTANBAWHSSC ->
MGSYLCSVPAYPTSRDP (in isoform LIMK2B,
isoform LIMK2B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS00478; LIM_DOMAIN_1; 2.
PROSITE; PS50023; LIM_DOMAIN_2; 2.
PROSITE; PS50103; DZ, 1.
PROSITE; PS01107; PROTEIN_KINASE_AFF; 1.
PROSITE; PS01108; PROTEIN_KINASE_ST; FALSE_NEG.
PROSITE; PS001108; PROTEIN_KINASE_DOM: 1.
Transferase; Serine/Throonine-Protein; kinase; AFP-binding; Repeat:: DOMAIN | 12 63 LIM 1.
                SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES. SIMILARITY: Contains 2 LIM zinc-binding domains. SIMILARITY: Contains 1 PDZ/DHR domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /FIId-vSP_003128
VTHKATACKWWWKELIKODEETOK -> SWE
OSDGIEGWNSL (in isoform LIMK2C)
/FIId-vSP_003129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (in isoform LIMK2C).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Missing (in isoform LIMK2D).
/FTId-VSP_003131.
A7E2D525751BE4F3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1; Length 638;
EXCEPT FOR TESTIS, WHICH SHOWS VERY LOW EXPRESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Zinc; Alternative splicing.
LIM 1.
LIM 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATP (BY SIMILARITY). ATP (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROTEIN KINASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /FTId=VSP_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 7;
                                                                                                                                                                                                                                                                                                                 InterPro: IPR001478; PD2.
InterPro: IPR000719; Prot_kinase.
InterPro: IPR002290; Ser_thr_pkinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Missing
                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00069; pkinase; 1.
Probom; PD000094; LIM; 2.
Probom; PD003001; Prot_kinase; 1.
                                                                                                                                                                                    EMBL, D31874; BAA06673.1; --
EMBL, D31875; BAA06674.1; --
EMBL, D31875; BAA06675.1; --
EMBL, D31877; BAA06676.1; --
PIR; I78846; I78846.
PIR; I78848; I78847.
PIR; I78848; I78847.
PIR; I78848; I78847.
PIR; I78848; I78848.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     638 AA; 72202 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21.2%;
100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity luv.v.
T; Conservative
                                                                                                                                                                                                                                                                                                                                                           Pfam; PFC0412; LIM; 2.
Pfam; PF00595; PD2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        638
                                                                                                                                                                                                                                                                                                                                                                                                                                  SMART; SM00132; LIM; 2
SMART; SM00228; PDZ; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BINDING
ACT_SITE
VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
NP_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tob I., Alba H., Baba I. Fujita K., Hayashi K., Inada T., Isono K., Kasai H., Kimura S., Kitakawa M., Kitagawa M., Makaino K., Makii T., Mizobuchi K., Mori H., Mori T., Motomura K., Nakade S., Nakamura Y., Nashimoto H., Nishic Y., Oshima T., Saito N., Sampel G., Seki Y., Sivasundaram S., Tagami H., Takeda J., Takemoto K., Wada C., Yamamoto Y., Horiuchi T., Hariothi T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEMS Microbiol. Lett. 149:115-120(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Link A.J., Robison K., Church G.M.; "Comparing the predicted and observed properties of proteins encoded in the genome of Escherichia coli K-12."; Electrophoresis 18:1259-1313(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                determines colony morphology and autoaggregation in Escherichia coli
                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAINKIZ, / MG1655,
MEDLINE=97426617; Pubked-9278503;
Matting F.R., Plunkett G. III, Bloch C.A., Perna N.I., Burland V.,
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FUNCTION AS AN ADHESIN.
-!- SUBUNIT: HETERODIMER OF THE PERIPHERAL MEMBRANE PROTEIN (ALPHA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Caffrey P., Owen P.;
Purification and N-terminal sequence of the alpha subunit of amina
43, a unique protein complex associated with the outer membrane of
Escherichia coli.";
                                                                                                                                                                                        Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriaies;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CHAIN) ANCHORED TO THE INTEGRAL OUTER MEMBRANE PROTEIN (BETA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Henderson I.R., Meehan M., Owen P.;
"Antigen 43, a phase-variable bipartite outer membrane protein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -:- SUBCELLULAR LOCATION: Outer membrane-associated.
-:- SIMILARITY: TO ADHESIN AIDI-I AND TO BORDETELLA PERTACTIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "The complete genome sequence of Escherichia coli K-12.";
Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-ML 308-225;
Bonderson 1.R., Owen P.;
Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
01-FEB-1995 (Rel. 31, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Antigen 43 precursor (AG43) (Fluffing protein).
FLU OR B2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN~ML 308-225;
MEDI/INE=89291704; PubMed~2661530;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteriol. 171:3634-3640(1989)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-K12 / EMG2;
MEDLINE-97443975; PubMed-9298646;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=97257509; PubMed=9103983;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=97251358; PubMed=9097040;
                                                                                                                                                                                                                     Enterobacteriaceae; Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY SEQUENCE OF 53-78.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA Res. 3:379-392(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 53-63.
                                                                                                                                                     Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mau B., Shao Y.;
                                                                                                                                                                                                                                                     NCBI_TaxID=562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENE NAME
```

ö

Gaps

ċ

0; Indels

Mismatches Pred. No.

:

AG43_ECOL: ID AG43_ECOLI STANDAKD; PRT: 1039 AA. AC P39180; P75614; P76360; P97241; Q46771;

RESULT 9

ô d

```
TISSUE-Testis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ransmembrane.
                                                                                                                                                                                                                                                                                                                                                                       TY13_HUMAN
Q9BZ97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YG12_BACHD
ID YG12_BACHD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ocery Match
                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                             TY13_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 12
      use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for connerrial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      :
ن.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      pisum sativum (Garden pea).
Eukaryota: Viridiplantae: Streptophyta; Embryophyta; Tracheophyta:
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Vicicae; Pisum.
NCBI_TaxIb=3888;
                                                                                                                                                                                                                                                                ANTIGEN 43 BETA CHAIN.

K -> N (IN STRAIN ML 308-225).

SL -> FF (IN STRAIN ML 308-225).

T -> X (IN STRAIN ML 308-225).

W -> L (IN STRAIN ML 308-225).

W -> L (IN STRAIN ML 308-225).

AIN -> SI (IN STRAIN ML 308-225).

AIN -> T (IN STRAIN ML 308-225).

AIN -> T (IN STRAIN ML 308-225).

N -> Q (IN STRAIN ML 308-225).

E -> V (IN STRAIN ML 308-225).

H -> Y (IN STRAIN ML 308-225).

E -> X (IN STRAIN ML 308-225).

C -> S (IN STRAIN ML 308-225).

A -> V (IN STRAIN ML 308-225).

C -> S (IN STRAIN ML 308-225).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last Sequence update)
8-FEB-2003 (Rel. 41, Last annotation update)
Photosystem I reaction center subunit V (PSI-G) (P)otosystem I 9 kDa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    225).
QGT -> LGA (IN STRAIN ML 508-225).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      с
:.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            55 S -> T (IN STRAIN M. 308-225).
89 0 -> L (IN STRAIN M. 308-225).
25 S -> I (IN STRAIN M. 308-225).
63 EIV -> ITT (IN REY. 5).
10684: MW. 5170F647CRDEBREC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1: Length 1659:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    S; Indeis
                                                                                                                                                                                                                                                       ANTIGEN 43 ALPHA CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          39 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                              TTCRFAMS; TICR01414; autotrans_barl; 1.
Cuter membrane; Signal; Complete proteome.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21.2%; Score 7;
100.0%; Pred. No
                                                                EMBL, AE000291, AAC75061.1; ALT_INIT.
EMBL, D90838; BAA15825.1; AIT_INIT.
EMBL, D90839; BAA15832.1; ALT_INIT.
EMBL: C24429; AAB47869.1; -.
HSSP; P07505; 1SRD.
                                                                                                                                Ecodene; Ed12686; flu.
InterPro; ERR066315; Autotransport.
InterPro; IPR005636; Autotransporter.
InterPro; IPR004899; Perfactin.
                                                                                                                                                                                     Pfam: PF03797; Autotransporter; 1.
Pfam: PF03212; Pertactin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match
Best Local Similarity Tousers
The 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 6
1039 AA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1111111
36 VAVALS:: 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 VAVALSL 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              855
888
1025
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PSAG_PEA
P20120;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VARIANT
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                     CHAIN
CHAIN
VARIANT
VARIANT
VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VARIANT
VARIANT
VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VARIANT
VARIANT
                                                                                                                                                                                                                                                                                                                                              VARIANT
VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                        VARIANT
VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VARIANT
                                                                                                                                                                                                                                                                                                                                                                        VARIANT
                                                                                                                                                                                                                                                                                                                                                                                     VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                    VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                               VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                          VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PSAG_PEA
 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NEW COCCOCC
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstation the European Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ċ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ်
                                                                                                                                                                                                                                                                                                               Interpro: IPR000549; PSI_PSaG/K.
Pfam: PF01241: PSI_PSAK: 1.
PR027E: PS01026: PH0TOSYSTEM_I_PSAGK; PARTIAL.
Photosy:thesis; Photosystem I: Transmembrane: Chloroplast: Thylakoid.
NON_IER 39 39
SEQUENCE 39 AA: 4397 MW: 00EEBA9E219D91A3 CRC64:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kuroda-Kawaguchi T., Skaletsky H., Minx P.J., Brown I.G., Rozen S. Wilson R.K., Waterston R.H., Page D.C.; "The DNA sequence of the human Y chromosome."; Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human).
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Eutelcostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                 FEBS_Cett. 228:157-161(1988).
-:- FUNCTION: NOT YET KNOWN.
-:- SURCELLUIAR LOCATION: Integral membrane protein. Chloroplast thylakoid membrane (Probable).
-:- SIMILARITY: Belangs to the psaG / psak family.
-:- SIMILARITY: Belangs to the psaG / psak family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
MEDLINE-89137587; PubMed-3277857;
Dunn P.P.J., Packman L.C., Pappin D., Gray J.C.;
"N-terminal amino acid sequence analysis of the subunits of
photosystem I.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18.2%; Score 6; DB 1; Length 39;
100.0%; Pred. No. 19;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     58 AA; 6256 MW; F714A679F062DFE1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28-FED-2003 (Rel. 41, Created)
28-FED-2003 (Rel. 41, Last sequence update)
28-FED-2003 (Rel. 41, Last annotation update)
TITY13 OR TIY13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18.2%; Score 6; DB 1;
100.0%; Pred. No. 26;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              111 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AF332242; AAK13492.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Genew; HGNC:18494; TTTY13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 100.
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 100.
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5 LSLFLG 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5 LSLFLG 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID-9606;
```

```
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AF043498; AAC39607.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12912 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18.28;
                                                                                                                                                                           Oncodene 19:1288-1296(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cuery Match
Best Local Similarity
5: Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              111 PALGLL 116
                                          TISSUE SPECIFICITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22 PALGIL 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DISULFID
DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LIPID
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DISULFID
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROPER
                                                                                                                                                             cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NIAMOU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GTH2_MORSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      688888
      qq
                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the SWISS institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for connectial entities requires a license agreement (See attp://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ç,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE-Prostatic carcinoma;
MEDLINE-99132661; PubMed=9465086;
Reiter R.E., Gu 2., Watabe T., Thomas G., Szigeti K., Davis E.,
Wahl M., Nisitani S., Yamashiro J., le Beau M.M., Losa M., Witte O.N.;
"Prostate stem cell antigen: a cell surface marker overexpressed in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     841.8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bahrenberg G., Joost H.G.;
"Serial analysis of the gene expression of a highly differentiated
urothelial tumor.";
                                                                                                                                                                                                                                                                                                        "Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and genomic sequence comparison with Bacillus subtillis. Nucleic Acids Res. 28:4317-4331(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bukaryota, Metazoa, Chordata, Craniata, Vortebrata, Eutelcostomi;
Mammalia, Eutheria, Primates, Catarrhini, Sominidae, Homo.
                                                                                                                                                                                                                                                   Takami H., Nakasone K., Takaki Y., Maenc G., Sasaki R., Masui N.
Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           08 1; Length 111;
                                                                                                                    Bacteria; Firmicutes; Bacillaics; Baciliaceae; Bacilius.
NCBI_TaxID=86665;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0: Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hypothetical protein: Complete protecme.
SEQUENCE 111 AA: 12782 MW; 24730C750C2096EE CRC54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           prostate cancer.";
Proc. Natl. Acad. Sci. U.S.A. 95:1735-1740(1998)
              16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last Sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Hypothetical protein BH1612.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18.2%; Score 6; DB 1
100.0%; Pred. No. 42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             123 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Pred. no.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence u
16-0CT-2001 (Rel. 40, Last annotation
Prostate stem cell antigen precursor.
                                                                                                                                                                                                                                 MEDLINE-20512582; PubMed-11058132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AP001512; BAB05331.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      rik, Dosmai, Dosmai.
InterPro, IPR005347; UPF0131.
Pfam; PF03674; UPF0131; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 100.
Matches 6; Conservative
                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN-C-125 / JCM 9153;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human)
                                                                                                                  Bacillus halodurans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PIR; D83851; D8385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19 GYPAL 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22 LGYPAL 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE-Urothelial;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID-9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         prostate cancer
                                                                                                                                                                                                                                                                    Fuji F., Hiran
Horikoshi K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PSCA_HUMAN
043653;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                BH1612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PSCA_HUMAN
ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LID DAY OF THE REPORT OF THE T
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bicinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its mac by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ó
                                                                                                                                                                                                                                                     -:- SUBCELLUIAR LOCATION: Attached to the membrane by a GPI-anchor.
-:- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN PROSTATE (BASAL, SECRETORY AND NEUROENDOCRINE EPITHELLUM CELLS). ALSO POUND IN BLADDER (TRANSITIONAL EPITHELLUM), PLACENTA (TROPHOBLASTS), STOWACH (NEUROENDOCRINE CELLS), COLON (NEUROENDOCRINE CELLS) AND KIDNEY (COLLECTING DUCTS). OVEREXPRESSED IN PROSTATE CANCERS AND EXPRESSION IS CORFLATED WITH TUMOR STAGE, GRADE AND ANDROGEN-INDREPRINENCE. HIGHLY EXPRESSED IN PROSTATE CANCER BONE METASTAGES.
MEDLINE-20180504: PubMed-10713670;

Gu Z., Thomas G., Yamashiro J., Shintaku I.P., Dorey F., Raitano A.,

Witte O.N., Said J.W., Loda M., Reiter R.E.;

"Prostate stem cell antigen (PSCA) expression increases with high

gleason score, advanced stage and bone metastasis in prostate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-LINKED (GLCHAC. ..) (POTENTIAL).
N-LINKED (GLCHAC. ..) (POTENTIAL).
N-LINKED (GLCHAC. ..) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REMOVED IN MATURE FORK (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      :.
ت
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 123;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSTATE STEM CELL ANTIGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL, AJ297436; CAB97347 1; Conew, HGNC:9500; FSCA.
MIM, G02470; Ciplasma membrane; TAS.
G0; G0:000886; C:plasma membrane; TAS.
G0; G0:000822; F:tumor antigen; TAS.
InterPro; IPR00342; Ly-6_CD59.
InterPro; IPR00342; Ly-6_CD59.
InterPro; PD003128; Ly-6_CD59; L.
SMART; SM00134; Ly-1, L.
SMART; M00134; Ly-1, L.
SMART; PS00983; Ly-6_UDAR; FALSE_NEG.
Signal; Antigen; Glycoprotein; Membrane; GP1-anchor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GPI-ANCHOR (POTENTIAL).
3FC1271742D657FA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GTH2_MORSA STANDARD; PRT: 139 AA.
091121;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Gonadotropin beta-II chain precursor (GTH-II-beta).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. 45;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                UPAR/LY6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 5;
```

9

```
SECUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Transit peptide
                                                                                                                                                                                                                                                                                                                          thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CHAIN
  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Ricinformatics and the EMBL outstation-the European Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ë
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Arabidopsis thallana (Mouse-ear cress).

Eukaryota: Viridiplantae: Streptophyta: Embryophyta; Tracheop.y.a:
Spermatophyta: Magnoliophyta: eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.

NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Saps
         Eukaryota; Metazoa; Chordata; Graniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Percoidei;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PSAG_ARATH STANDARD: PRI; 160 AA. 09S7N7: 042310; 28-FEB-2003 (Rel. 41, Created) 28-FEB-2003 (Rel. 41, Last sequence update) 28-FEB-2003 (Rel. 41, Last annotation update) Photosystem I reaction center subunit V, chloropiast precursor (PS)-
                                                                                       TISSUE-Pituitary;
MEDLINE-96020549; PubMed-8546811;
Hassin S., Elizur A., Zohar Y.;
"Molecular cloning and sequence analysis of striped bass (Morche saxatilis) gonadotrophin-I and -II subunits.";
J. Mol. Endocrinel. 15:23-35(1995).
                                                                                                                                                          -:- FUNCTION: INVOLVED IN SAMETHOGENESIS AND STEROIDDOGENSIS.
-:- SUBUNIT: Heterodimer of an alpha and a beta chain.
-:- SIMILARITY: BELONGS TO THE GLYCOPROFEIN HORMONES BETA CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .) (POIENTIAL.)
                                                                                                                                                                                                                                                                                                                                                                                                                                           GONALCTROPIN BETA-II CHAIN.
BY SIMILARITY.
W. INKED (GICNAC. . .) (POIEN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1; Length 139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PSAG OR ATIG55670 OR F20N2_3 OR F20N2.33 OR F20N2.21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Pred. ...
ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE: PS00261; GLYCO_HORMONE_BETA_1; PROSITE; PS00689; GLYCO_HORMONE_BETA_2; Hormone: Glycoprotein: Signai.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18.28; Score 6;
                                                                                                                                                                                                                                                                                                         EMBL: 135096; AAC38019.1; ALT_INIT.
                                                                                                                                                                                                                                                                                                                            InterPro: IPR006208; Cys.knot.
InterPro: IPR002400; GF_cysknot.
InterPro: IPR001545; Gly_hormoneB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15555 MW;
                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00007; Cys_knot; 1. PRINTS; PR00438; GFCYSKNOT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                    24
139
78
93
131
109
111
121
                                                                                                                                                                                                                                                                                                                                                                                      SMART; SM00068; GHB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  244
444
555
1114
134
139 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
es 6; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5 LSLFLG 10
                                             Moronidae, Morone.
NCBI_TaxID=34816;
                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                              FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DISULFID
DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                        DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                    SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PSAG_ARATH
ID PSAG_AR
DT 28-FEB
DT 28-FEB
DE Photosi
DE G)
OS Arabido
OC Eukary
OC Eukary
OC eurosi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Loc
Matches
g
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Baloinformatics and the EMBL outstation the European Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S., Maite O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brocks S.Y., Buehler E., Chan A., Chao Q., Chao H., Cheuk R.F., Chin C.W., Chan M., Coon L., Conway A.B., Conway A.R., Creasy T.H., Dewar K., Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K., Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizar L., Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E., Lin K., Ch. Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Il Y.-P., A. Lin X., Liu S.X., Luros J.S., Maith R., Marziali A., Lin X., Liu S.X., Luros J.S., Maith R., Marziali A., Miltscher J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I., A. Sakano H., Salzberg S.L., Shinn P., Southwick A.M., A. Sakano H., Salzberg S.L., Shinn P., Southwick A.M., A. Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D., Walker M., Wu D., Yu G., Fraser C.M., Vaysberg M., Vysotskaia V.S., Walker M., Sequence and analysis of chromosome I of the plant Arabidopsis
SEGUENCE FROM N.A.
STRAIN=cv. Columbia;
Legen J., Misera S., Herrmann R.G., Altschmied J..;
Legen D., Misera S., Herrmann R.G., Altschmied J..;
"Sequences and map position of 31 Arabidopsis thaliana conas encoding organellar polypeptides.",
organellar polypeptides.",
Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                pfam; PF01241; PSI_PSAK; i.
PROSITE; PS01026; PHOTOSYSTEM_I_PSAGK; 1.
Photosynthesis; Photosystem I; Transmembrane; Chloroplast; !hylakoid;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CHLOROPLAST (BY SIMILARITY).
PHOTOSYSTEM I REACTION CENTER SUBUNIT V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIRAIN-CV. Columbia:
Shinozaki K., Davis R.W., Ecker J.R., Theologis A.;
"RIXEN Arabidopsis full length cDNA clones (RAFLs) sequenced by the
SSP consortium (Salk/Stanford/PGEC).";
Submitted (JAN-2001) to the EMBI/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -:- FUNCTION: NOT YET KNOWN.
-:- SUBCELLULAR LOCATION: Integral membrane protein. Chloroplast.
thylakoid membrane (Probable).
-:- SIMILARITY: Belongs to the psas / psak family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (SEP-1994) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6EF23E57C7C50760 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-cv. Columbia;
Bardet C., Dabos P., Tremousaygue D., Lescure B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN-cv. Columbia;
MEDLINE-21016719; PubMed=11130712;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMEL: AJ245630; CAB52748.1; -.
EMEL: AC002328; AAC83069.1; -.
EMEL: AF326870; AAG41452.1; -.
EMEL: AF324710; AAG40061.1; -.
EMEL: AF339622; AAK00574.1; -.
EMEL: AF339622; AAK00574.1; -.
EMEL: AF339627; AAK00574.1; -.
EMEL: AF330627; AAK00574.1; -.
EMEL: AF330627; AAK00574.1; -.
EMEL: AF330627; AAK00574.1; -.
EMEL: AF300574; -.
EMEL: A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17085 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 27-127 FRCM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nature 408:816-820(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                60
160
86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           160 AA;
```

18.2%; Score 6; DB 1; Length 160;

0; Gaps 0; Indels Best Local Similarity 100.0%; Pred. No. 54; Matches 6; Conservative 0; Mismatches 90

Ö

5 LSLFLG 10 ||||||||| 74 LSLFLG 79

Search completed: September 26, 2003, 17:37:20 Job time : 4.93192 secs

Q9ltn3 tupaia herp

12 Q91TN3

221

21.2

۲-

17

```
September 26, 2003, 17:28:45; Search time 17:1319 Seconds (without alignments) 497:069 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              830525
GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-852-100A-2_COFY_185_217
33
1 VAVALSLEIGWIGADRFYLGYPALGIIKFCTVG 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           830525 seqs, 258052604 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Post-processing: Listing first 45 summaries
                                                                                                                                                                                                                             OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SPTREMBL_23:*

1: Sp_archea:*
2: Sp_barchea:*
3: Sp_fungi:*
4: Sp_human:*
5: Sp_mammal:*
5: Sp_mammal:*
5: Sp_phore:*
6: Sp_phor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OLIGO
Gapop 60.0 , Gapext 60.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sp_rodent:*
sp_virus:*
sp_virus:*
sp_vorlassified:*
sp_roinus:*
sp_bacteriap:*
sp_archeap:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Title:
Perfect score:
Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Word size :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Database :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Searched:
                                                                                                                                                                                                                                                                                                                                     Run on:
```

					SUMMARIES		27	Smith S.C., Wood A., Rhodes K.J., Kennedv J.D.,	7. J.D.
		o <b>s</b> p	æ				RA	Jacobsen J.S., Ozenberger B.A.;	•
		Query					ir.	"beta-Amyloid Peptide-Induced Apoptosis Regulat	Requiat
No. So	core	Match	Length	038	ID	Description	E-	Containing a G Protein Activation Module.";	
				:		1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	 	J. Biol. Chem. 276:18748-18756(2001).	
-	33	100.0	207	4		OSbx74 homo sapies	Z (X	. 2 ]	
2	33	100.0	208	11		Q99mb3 mus musculu	ik.	SECUENCE FROM N.A.	
m	ထ	24.2	8.0	4	0	Deh046 home sapies	5 6.	TISSUE=Testis;	
4	œ	24.2	178	S		J9w2hl dresophila	RA	Strausberg R.:	
S	œ	24.2	195	2		955qz5 caenorhabdi	RL	Submitted (MAY-2002) to the EMBL/GenBank/DDBJ d	/DDBJ o
Q	œ	24.2	221	4		09h651 homo sapien	DR	EMBL; AF353990; AAK35064.1;	
7	80	24.2	230	11		09d156 mus muscula	SC	EMBL: BC029486; AAH29486.1;	
œ	œ	24.2	247	4	0	Ogbrn9 home sapien	KW	Signal	
on	00	24.2	261	Ξ		O8bj83 mus musculu	FT	SIGNAL 1 37 POTENTIAL.	
10	œ	24.2	284	ß.		Ogu4h5 drosophila	SO	SEQUENCE 207 AA; 22326 MW; A5590FD7AECDF292	ECDF292
11	7	21.2	38	Ξ		OBcaml mus musculu			
12	7	21.2	150	16		OBevi7 mycoplasma	0	Ouerv Match 100.0%: Score 33:	DB 4:
13	7	21.2	159	10		O9ixv9 arabidossis	r sti	Best Local Similarity 100.0%; Pred. No. 2.1e-24	2.1e-24
14	7	21.2	180	16		OBfov7 corvnebacte	Σ	Matches 33: Conservative 0: Mismatches	les (
15	7	21.2	194	16		092qw4 rhizobium m			
16	7	21.2	219	16	O9RXIO Q9r	O9rxi0 deinococcus	δò	1 VAVALSLFLGWLGADRFYLGYPALGLLKFCTVG 33	.VG 33

A. 25.1 1.2 2.2 25.1 1.2 2.2 25.3 1.6 2.2 3.3 1.6 2.2 3.3 1.6 2.2 3.3 1.6 2.3 1.6 2.3 1.6 2.3 1.6 2.3 1.6 2.3 1.6 2.3 1.6 2.3 1.6 2.3 1.6 2.3 1.6 2.3 1.6 2.3 1.6 2.3 1.6 2.3 1.6 2.3 1.6 2.3 1.6 2.3 1.6 2.3 1.6 2.3 1.6 2.3 1.6 2.3 1.6 2.3 1.6 2.3 1.6 2.3 1.6 2.3 1.6 2.3 1.6 3.3 1.3 1.3 1.3 1.3 1.3 1.3 1.3 1.3 1.3	OBDESS4 mus musculu OBDESS4 mus musculu OBDESS4 cus observation ob	Uydalwy Streptococc 093til streptococc 093til streptococc 093til streptococc 08650 streptococc 086422 streptococc 086422 streptococc 097430 delnococcus 09748 arabidopsis 089vy8 arabidopsis 089vy8 arabidopsis	rs 7 n.a.	ce update) Lion update)	Vertebrata; Euteleostomi; i; Hominidae; Homo.	X., Walker S., Sofia H.J., Wang W., Y., Vile S., Ryan K., McHendry-Rinde B., J., Kennedy J.D., Bard J., Apoptosis Regulated by a Novel Protein. tion Module.";	MBL/GenBank/DDBJ databascs. POTENTIAL. A5590FD7AECDF292 CRC64;	DB 4; Length 207; 2.1e-24; hes 0; Indels 0; Gaps 0;
PRELIN PRELIN COLD (TTERM COLD		100 100 100 100 100 100 100 100 100 100	ALIGNMENT	urel. i7, Created) Nrei. 17, Last sequence update) Nrei. 22, Last annotation updat. ng protein	nn). 1; Choùdata: Craniata; Vertebrat 1; Primates; Catarrhini; Hominid	Pubbacd=11278849; C.F., Ning X., Walken C.F., Roder E., Vile S., A., Rhodes K.J., Kennec suberger B.A., ide-induced Apoptosis stein Activation Modul S:18748-18756(2001).	<ul> <li>12) to the EMBL/GenBank/DDBJ databasus NK35064.1;</li> <li>NE29466.1;</li> <li>POTENTIAL.</li> <li>22326 MM; ASS90FD7AECDF292 CRC64;</li> </ul>	.0%; Score 33; .0%; Pred. No. 0; Mismatc
RESULT 1 098874 00 00 00 00 00 00 00 00 00 00 00 00 00			RESULT 1 05BX74 1D Q9BX74 PRELIM	AC 09BX74.  03 01-JUN-2001 (TrEME)  01 01-JUN-2001 (TrEME)  01 01-CCT-2002 (TrEME)  05 Beta-amyloid bindi  3N BBP.	DS HOMO Sapiens (Hume OC Eukaryota; Metazoa OK Mammalia; Euthoria OX NCBL_TaxID=9606;	KAP SECUENCE FROM N.A. MEDLINE-21276355, SAF. Kajkowski E.W., LC EA Edris W., Chanda I. S.C., Wood P. S. Smith S.C., Wood P. S. Jacobsen J.S., Ozdera-Amyloid Pept ST. Tenta-Amyloid Pept ST. Containing a G Prom. 27, 31, Biol. Chem. 277	FR SECTENCE FROM N.A. FC TISSUE=Testis: FA Strausberg R.; RL Submitted (MAY-200; DR EMBL; AF353990; AA; EMBL; BC029486; AA; EMBL; BC029486; AA; EMBL; SCOURNE SIGNAL FT SIGNAL SCOURNE SOURNE 207 AA;	Query Match Best Local Similarity 100 Matches 33; Conservative

099MB3

ACCOS OCT NEW REARCE RE

```
K. STRATW-BERKLEY;

Addams M.D. Celniker S.E., Holt R.A. Evans C.A., Gocayne J.D.,

Addams M.D. Celniker S.E., Holt R.A. Evans C.A., Gocayne J.D.,

R.A. Addams M.D. Celniker S.E., Holt R.A., Edgle R.F.,

Gocaye R.A. Lewis S.E., Findards S. Amburner M., Henderson S.N.,

Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,

R. Brandon R.C., Rogers Y.-H.C., Blazel R.G., Champe M., Pfeiffer B.D.

R. Antil J.F., Aguiann J.R., Mandell M.D., Edgle B.D., Polyle C., Haldwin D.,

Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Reasley F.M.,

Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Reasley F.M.,

Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Peasley F.M.,

Ballew R.M., Cawley S., Dablke C., Dovenport L. B., Davies P.,

Burkova D. Botchen M.R., Bouck J., Brokstein P., Brottler P.,

Burkova D., M., Cawley S., Dablke C., Davenport L. B., Davies P.,

Burkova D., Doup L.E., Downes M., Dugan Rocha S., Fleischman W.,

R. Bondon K., Doup L.E., Downes M., Dugaser K.,

R. Doup L.E., Downes M., Davies P., Brits R.M.,

R. Doup L.E., Downes M., Davies P., Brits R.,

R. Gabrielian A.F., Gelbart W.M., Glasser K.,

R. Anthin K.J., Wougher F., Karpen G.H., W., Glasser R.,

Alali M., Kalush F., Karpen G.H., Re Z., Gubar P., Mrcherson D.L.,

Alali M., Kalush F., Karpen G.H., Mixon V. Morsher I. M.,

R. Markillow G., Milshian N.V., Mobarry C., Morris J., Moshrefi A.,

Alali M., Malush P., Rarpen G.H., Mixon W., Marsken D. B., Pari, Wang Y., Lin X.,

R. Mount S.L., Moy M., Murphy B., Murphy L., Muruy D.M., Nelson D.,

R. Spier E., Spradling A.C., Stapheron M., Stupski M.P., Smith T.,

Spier E., Spradling A.C., Stapheron M., Skupski M.P., Smith T.,

Spier E., Spradling A.C., Stapheron M., Skupski M.P., Smith H.O.,

R. Shies R. M., Morshey R., Wondey K.C., Wu D., Yang S., Yao O.A.,

R. Shies R. M., Morshey R., Wondey R., Wang S., Yao O.A.,

R. Spier E., Spradling A.C., Stapheron M., Stupski M.P., Smith H.O.,

R. Shere E., Spradling G.M., Weissenbach J.,

R. Shies R., Shore S., Ranning G.M., Weissenbach J.,

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-Berkeley;
Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
Nunco J., Pacleb J., Paragas V., Park S., Phouanenavong S., Wan K.,
Tu C., Lewis S.E., Rubin G.M., Celniker S.,
Submitted (OCT-2001) to hEMBL/GenBank/DDBJ databases.
EMBL; AR061343; AAL28891.1;
                                                                                                                                                                                                                       Eukaryota; Metazoa; Arthropoda; Hekapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Epkydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 8; DB 5; Length 178; Pred. No. 4.4; 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FIYBase; FBgn0034626; CG10795.
SEOUENCE 178 AA: 19896 MW; 17C41166607ACC03 CRC64;
                                                                                                                Last seguence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24.2%; Score 8;
                                                                                             Created)
                                                                                                                                                                                                      Drosophila melanogaster (Fruit fly)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 24.2%;
Best Local Similarity 100.0%;
Matches 8; Conservative 0
                                                                                      01-MAY-2000 (TrEMBLrel. 13,
C1-MAY-2000 (TrEMBLrel. 13,
C1-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                         CG10795 protein (LD27358P).
                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                             NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                  STRAIN-BERKELEY;
                                                                09W2H1;
                                                                                                                                                                                 CG10795
                                             09W2H1
                          O9WZH]
                                                                                                              ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kajkowski E.M., Lo C.F., Ning X., Walker S., Sofia H.J., Wang W., Edris W., Chanda P., Wagner E., Vile S., Ryan K., McHendry-Rinde B., Smith S.C., wood A., Rhodes K.J., Kennedy J.D., Bard J., Jacobsen J.S., Ozenborger B.A.; "betar-Amyloid Peptide-induced Apoptosis Regulated by a Novel Protein Containing a G Protein Activation Module."; J. Biol. Chem. 276:18748-18756(2021).
BMBL, ARSS9993; AAKSS067.1; ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata: Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 33; DH 11; Length 268; 100.0%; Pred. No. 2.2e-24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       H.W., Weil B., Wiemann S.;
EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22271 MW; 91A7932163F4F04C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE 80 AA; 8699 MW; 8BE6BE788235C58D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Last sequence update)
Last annotation update)
                                                                                                                                                                              01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TREMBLrel. 17, Last sequence update)
01-DEC-2001 (TREMBLrel. 19, Last annotation update)
Beta-amyloid binding protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 124 VAVALSLFLGWLGADRFYLGYPALGLIKFCTVG 156
                     123 VAVALSLFLGWLGADRFYLGYPALGLLKFCTVG 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 VAVALSLFLGWLGADRFYLGYPALGLLKFCTVG 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  80 AA.
                                                                                                                                   208 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. 2.2
0; Mismatches
Score 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAR-20C1 (TrEMBLrol. 16, Created)
01-MAR-20C1 (TrEMBLrol. 16, Last sequ
01-0CT-2002 (TrEMBLrol. 22, Last anno
BYPOThetical protein (Fragment).
DKF2P667C1011.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=BALB/c;
MEDLINE-21276355; PubMed-1:278849;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Koehrer K., Beyer A., Mewes
Submitted (DEC-2000) to the
EMBL: AL512689; CAC21647.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hypothetical protein.
                                                                                                                                                                                                                                                                                               Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13 GADRFYLG 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GADRFYLG 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                208 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
Matches 33; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      rISSUE=Lymph node;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID-9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9H046
Q9H046;
                                                                                                                                   Q99MB3
```

RESULT 3 **29H046** 

1D DTTDDTTDDT DDTTDDT DDTTDDT DDTTDDT SCOCC SCOC

qq δ

0

Gaps

0;

```
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hayashizaki Y.;
                                                                                                                                                                                                                                                      TISSUE-Muscle;
                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 7
09D156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     d
      ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ÷
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sape
                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoldeu:
Rhabditidae; Peloderinae; Caenorhabditis.
NCBL_TaxID-6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Small intestine;
Watanabe K., Kumagai A., Itakura S., Yamazaki M., Tashiro H., Ota
Suzuki Y., Obayashi M., Nishi T., Shibahara T., Tanaka T.,
Nakamura Y., Isogai T., Sugano S.;
"NEDO human cDNA sequencing project.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapions (Human).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarchini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Genome sequence of the nematode C. elegans: a platform for
investigating biology. The C. elegans Sequencing Consortium.";
Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24.2%: Score 8; DB 5; Length 195; 100.0%; Pred. No. 4.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gattung S., Maggi L.; The sequence of C. elegans cosmid C41D11."; Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases. EMBL; AF003740; AAL08031.1; ... WormPep; C41D11.9; CE29489.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hypothetical protein.
SEQUENCE 195 AA: 21203 MW: 35945E467F184DAE CRC64;
                                                                                                                                                                                                       01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
10-DEC-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical 21.2 kba protein.
C41011.9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Hypothetical protein FLJ22604 (BBP-like protein 2).
                                                                                                                                                                   195 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  221 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-Bristol N2;
MEDLINE-99069513; PubMed-9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ::
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                              Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'Direct Submission.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DRFYLGYP 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13 GADREYIG 20
                         DRFYLGYP 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. STRAIN-Bristol N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-Bristol N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID-9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Waterston R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ..
89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                         15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   09н651:
                                                                                                                                                                   095025
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    09H651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                            RESULT 5
Q95QZ5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 09H651
                                                                                                                                                                     DDE DATE OF THE BEAR AND THE BE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    q
                                                                  Ωp
```

```
Arakaya T., Hara A., Shibata K., Yoshino M., Itoh M., Ishii Y., Arakaya T., Hara A., Fukunishi Y., Konno H., Adachi J., Eukuda S., Arakaya T., Hara A., Fukunishi Y., Konno H., Adachi J., Eukuda S., Aizawa M., Nishi K., Konno H., Kondo S., Yamanaka I., Saito T., Oxazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., Kadota K., Matsuda H.A., Ashburnar M., Patalov S., Casavant T., Kuchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Mashio T., Satai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Baka J., Bult C., Fletcher C., Fujita M., Gariboidi M., Savai K., Marchlonni L., Mashima J., Mazzarelli J., Mombaerts P., Nordone P., Ring B., Rughald M., Rodriguez I., Sakamoto N., Sasaxi H., Sato K., Schocnbach C., Seya T., Shibala Y., Storik K., Wang K.H., Weitz C., Whittaker C., Wilming L., Mashima K., Weitz C., Whittaker C., Wilming L., Washima K., Weitz C., Whittaker C., Wilming L., Washima K., Wawaji H., Kohtshik S.,
SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

Kajkwaki E.M., Lo C.F., Ning X., Walker S., Sotia H.J., Wang W.,

Kajkwaki E.M., Lo C.F., Ning X., Walker S., Sotia H.J., Wang W.,

Smith S.C., Wood A., Rhodes K.J., Rennedy J.D., Bard J.,

Jacobsen J.S., Ozenberger B.A.,

"Beta-amy_cid peptide-induced apoptosis regulated by a novel protein
J. Biol. Chem. 0:0-0(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (Mouse).
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            o;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24.2%; Score 8; DB 4; Length 221; 100.0%; Pred. No. 5.3; ative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE-Salivary gland;
Strausberg R.;
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AK003917; BAB23075.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Strausberg R.;
Submitted (MAY-2001) to the EMBL/Genbank/DDBJ databases.
EMBL; AK026257; BAB15415.1; -.
EMBL; AF8559921; AAK35066.1; -.
EMBL; BC008873; AAH08673.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               221 AA; 24410 MW; 92151D6EF6363D74 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                09D156 PRELIMINARY; PRT; 230 AA. 09D156, 0.1-30W-2001 (TrEMBLrel. 17, Created) 01-30W-2001 (TrEMBLrel. 17, Last sequence update) 01-30W-2002 (TrEMBLrel. 21, Last annotation update) 11100251091k protein (RIKEM cDNA 11100251099 gene).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-C57BL/6J; TISSUE-Embryo;
MEDLINE=21085660; PubMed-11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13 GADRFYLG 20
                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SECUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID-10090;
```

.; O

214 GADRFYLG 221

a

MGD; MGI:1915884; 1110025109Rix. SEQUENCE 230 AA; 25639 MW; 396D650D8BEE99A5 CHC64;

EMBL; BC024620; AAH24620.1;

Best Loc Matches

O9BRN9

RESULT 8 O9BRN9

```
Adams M.D., Celniker S.E., Hoit R.A., Evans C.A., Gocayne J.D.,
Adams M.D., Celniker S.E., Hoit R.A., Evans C.A., Gocayne J.D.,
Adams M.D., Celniker S.E., Hoit R.A., Evans C.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Ashburnar M., Hendorson S.N.,
B. Sutton G.G., Wortnern J.R., Yandell M.D., Zhang O., Chen L.X.,
Brandon R.C., Rogers Y.-H.C., Blazej R.G., Chempe M., Pfeiffer B.D.,
R.A. Abrill J.F., Apbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
Ballew R.M., Basus A.M., Baxendale J., Bayraktarogis L., Beasloy E.W.,
Ballew R.M., Basons P.V., Berman B.P., Bhandari D., Boishakov S.,
Borckova D., Botchban W.R., Bouck J., Blandari D., Boishakov S.,
Borkova D., Botchban W.R., Bouck J., Browstein P., Fortier P.,
Burtis K.C., Busam D.A., Buller H., Cadieu E., Center A., Chandra I.,
Aurtis K.C., Busam D.A., Buller H., Cadieu E., Center A., Chandra I.,
Burtis K.C., Busam D.A., Buller H., Cadieu E., Center A., Chandra I.,
Bockon K., Doup L.E., Downes M., Dugan-Rocha S., Drakov B.C., Durin P.,
Bosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
A bosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
A houston K.J., Harvey J., Hernandez J.R., Houck J.,
Harris N.L., Harvey J., Helman T.J., Hernandez J.R., Houck J.,
Houston K.A., Gong F., Gorrell J.H., Ke Z., Kennison J.A., Ketchum K.A.,
A Hostin D., Houston K.A., Howland T.J., Wanny D.M., Nelson D.M.,
R.M. Mannel B.E., Kodira C.D., Krappen G.H., Kazvitz S., Kulp D., Lal Z.,
Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
Anderi B., McIntosh T.C., McLeod M.P., McPherson D.,
R.A. Balazolo M., Pittman G.S., Pan S., Pollard J., Wanny K., Barazolo M., Pittman G.S., Pan S., Pollard J., Wang X.,
Rabie B.C., Siden Klamos I., Simpson M., Skupski M.P., Smith T.,
Rabie B.C., Siden Klamos I., Simpson M., Skupski M.P., San L.,
Rabie B.C., Siden Klamos I., Simpson M., Skupski M.P., San L.,
Rabier B. Speicer M., Wooder T., Wooder S., Pan S.,
                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
Rubin G.W., Wan K.H., Harvey D., Lewis S.E., Brokstein P., Tsang G., Apbayani A., Arcaina T.T., Baxter E., Blazej R.G., Butenhoff C., Charpe M., Chavez C., Chew W., Doyle C.M., Farfan D.E., Frise E., Galle R., George R.A., Harris N.L., Hoskins R.A., Evans-Holm M., Houston K.A., Hummasti S.R., Kim E., Li P., Moshrefi M., Pacleb J.M., Park S., Sequeira A., Sethi H., Snir E., Svirskas R.R., Weinburg T., Celriker S.E.
                                                                                                                                                                                                 Drosophila melanogaster (Fruit fly).

Eukaryota: Metazoa: Arthropoda: Hexapoda: Insecta: Pterygota: Neoptera: Endopterygota: Diptera: Brachycera: Muscomorpha: Ephydroidea: Drosophilidae: Drosophila: NCBL_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Micheliod M.'A.E., Remillieux N.C., Randsholt N.B.; "Characterization of almondex."; Submitted (MAY-2000) to the EMBL/GenBank/DDBC databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Full Length Drosophila melanogaster cDNA sequence.";
Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases
                                                                                   01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                          284 AA
                                                                                                                                                      BCDNA.GH02974 (ALMONDEX) (AMX protein).
AMX OR BCDNA.GH02974 OR CG12127.
                                        PRT;
                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-BERKELEY;
                                                                  09U4H5; 09W361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    [ISSUE-Ovary;
                                             09U4H5
RESULT 10
0904H5
                                                                                                             S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     :)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The FANTOM Consortium,
the RIKEN Genome Exploration Research Group Phase 1 s II Team:
"Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNs.";
Nature 420:563-573(2002).
EMBL: AK077858: BAC37037.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                  Saps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (Mouse).
Eukaryota, Metazou: Chordata, Craniata, Vertebrata; Eutelcostomi;
Mammalia; Eutheria: Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                               Rukaryota, Metazoa; Chordata; Craniata; Vertebrata; Eutoleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                  ċ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               <u>:</u>.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24.2%; Score 8; DB 11; Length 261: 100.0%; Pred. No. 6.1; tive 0; Mismatches 0; Indels
                     score 8; DB 11; Length 230;
Pred. No. 5.5;
Mismatches C; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 247;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Strausberg R.;
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, BC006150; BC006150.1; -.
Hypothetical protain.
SEQUENCE 247 Aa; 27161 MW. CF1D0D9C53DDF73C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 37037.1; -.
28880 MW; 70346780D3CF5CDB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QBBJ83;
01-MAR-2003 (TrEMBLre. 23, Created)
01-MAR-2003 (TrEMBLre. 23, Last sequence .pdatc)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                              01-00N-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 8; DB 4;
Pred. No. 5.9;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           261 AA
                                                                                                                                                                                                                                                                                                                                                                                        Similar to hypothetical protein FLJ22604.
              24.2%; Score 8; E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT:
                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-C57BL/6J; TISSUE-FOrelimb;
MEDLINE-22354683; PubMed-12466851;
                     24.2°,
100.0%; Pre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similar to BBP-like protein 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24.2%; 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.v.
Best Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ouery Match
Best Local Similarity 100.0
                                             Local Similarity 100.
Les 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           200 GADRFYLG 207
                                                                                                                                                           183 GADRFYLG 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13 GADRFYLG 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13 GADRFYLG 20
                                                                                                                13 GADRFYLG 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID-10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE * Colon;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                       Query Match
                                                                                                                                                                                                                                                                                                OBBRN9:
```

088783

RESULT 9 Q8BJ83

Saps

.; C

```
Arabidopsis thaliana (Mouse-ēar cress).
Eukaryota: Viridiplantae; Streptophyta: Embryophyta: Tracheophyta;
Spermatophyta: Magnoliophyta: eudicotyladons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SERAIN-CV. Columbia;
STRAIN-CV. Columbia;
Seki M., Iida K., Satou M., Sakurai T., Akiyama K., Ishida J.,
Seki M., Iida K., Satou M., Sakurai T., Akiyama K., Ishida J.,
Nakajima M., Enju M., Kamiya A., Narusaka M., Carninci P., Kawai J.,
Hayashizaki Y., Shinozaki K.;
"Arabidopsis thaliana full-length cDNA.";
Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databascs.
EMBL; AL163975; CAB8818.];
EMBL; AK116643: BAC4329.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Jordan N., Bangert S., Wiedelmann R., Voss H., Unseld M., Mewes H.W. Rudd S., Lemcke K., Mayer K.F.X., Quetier F., Salanoubat M.; Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Corynebacterium efficiens.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Corynebacteriaceae; Corynebacterium.
NCBI_TaxID-152794;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21.2%; Score 7; DB 10; Length 159; 100.0%; Pred, No. 36; tive 0; Mismatches 0; Indels
                                                                                                                                               21.2%; Score 7; DB 16; Length 150;
                                                                                                                                                                                               indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EU Arabidopsis sequencing project;
Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases
    intracellular bacterial pathogen in humans.";
Nucleic Acids Res. 30:5293-5300(2002).
EMBL. AP004172: BAC4437.1;
"Hypotherical protein: Complete proteome.
SEQUENCE 150 AA; 17289 MW; 0FF392EB9F32F1F1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hypothetical protein.
SEQUENCE 159 AA: 17059 MW: A3F0A7B03B5AB78A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-WAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                           159 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ₹
                                                                                                                                                           100.08; Pred. ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hypothetical protein.
T1583_160 OR AT3G44020/71583_160.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ilarity 100.0%; P. Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conserved hypothetical protein.
                                                                                                                         Omery Match
Rest Local Similarity 100.00
Feet Conservative
                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             94 ALSLFLG 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 ALSLFLG 10
                                                                                                                                                                                                                                           13 GADRFYL 19
                                                                                                                                                                                                                                                                      11::111
70 GADREYI, 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rest Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           [2]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chery Match
                                                                                                                                                                                                                                                                                                                                                                                                                              09LXV9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q8FPV7;
                                                                                                                                                                                                                                                                                                                                                                                                         69LXV9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QREPV7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CE1381
                                                                                                                                                                                                                                                                                                                                                        RESULT 13
C9LXV9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CBFPV7
         ð
                                                                                                                                                                                                                                                                                       CP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COCCOON ARREST AND ARREST AND ARREST AND ARREST ARR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OCC CONTRACTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The FANTOM Consortium,
the RIKEN Genome Exploration Research Group Phase I s II Team;
"Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs.";
Nature 420,563-573(2002).
EMBL; AK038530; BAC30030.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=22354719; PubMed=1246555;
Sasaki Y., Ishikawa J., Yamashita A., Oshima K., Konri T., Furuya K.,
Yoshino C., Horino A., Shiba T., Sasaki T., Hattori M.;
"The complete genomic sequence of Mycoplasma peretrans, an
                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Saps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi:
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria: Firmicutes: Mollicutes: Mycoplasmataceae: Mycoplasma.
NCBI_TAXID=28227;
                                                                                                                                                                                                                                                                                                               ..
C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                              Length 284;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                il; Length 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              d; Indels
                                                                                                                                                                                                                                                                                                               0: Indels
                                                                                                                                                             InterPro: IPR001304; Lectin_C.
PROSITE: PS00615; C_TYPE_LECTIN_1: 1.
SEQUENCE 264 Aa: 31364 MW; BFBBFFB5733AC851 CFC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NON_TER 1 1 1
SEQUENCE 38 AA: 4188 MW; 2DB363A494415D42 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
                Fire genome sequence of Drosophila melanogaster. Science 287:2185-2195(2000)

EMBL: AF181623; AAD55409.1;

EMBL: AF217797; AAF36924.2;

EMBL: AE003446; AAF46474.2;
Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LIM motif-containing protein kinase 2 (Fragment)
                                                                                                                                                                                                                                                                 Score 8; DB 5;
Pred. No. 6.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ź
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                138 11
111;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     150 AA
                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21.2%; Score 7; L
100.0%; Pred. No.
ive 6; Mismatch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. STRAIN-CS7BL/6J; TISSUE-Hypothalamus; MEDLINE-22354683; Pubmed-12466851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                               .;
                                                                                                                                                                                                                                                                 24.2%; S
100.0%;
                                                                                                                                                 FlyBase; FBgn0000077; amx.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ouery Match
Bost Local Similarity 100.
                                                                                                                                                                                                                                                            Query Match 24.2
Best Local Similarity 106.
Matches 8; Conservativo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAR-2003 (TrEMBLrel.
01-MAR-2003 (TrEMBLrel.
01-MAR-2003 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mycoplasma penetrans.
                                                                                                                                                                                                                                                                                                                                                                                                    237 GADREYLG 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hypothetical protein. MYPE5770.
                                                                                                                                                                                                                                                                                                                                                           13 GADRFYLG 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 ALSLFIG 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 ALSLFLG 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID-10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-HF-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OBCAM1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q8EV17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q8EVI7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OBCAMI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 12
Q8EVI7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 11
```

ö

```
.;
:
                                                                                                                                                                 Ċ
                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                  Gaps
SEQUENCE FWOM N.A.
SECULENCE FROM N.A.
STATIN-YS-314 / AJ 12310 / DSM 44549 / JCM 11189;
STRAIN-YS-314 / AJ 12310 / DSM 44549 / JCM 11189;
STRAIN-YS-314 / AJ 12310 / DSM 44549 / JCM 11189;
Ikeo K., Suzuki M., Mashima J., Hino Y., Kikuchi H., Nakamura Y., Usuda Y., Sugimono S.;
The entire genomic Squence of Corynebacterium efficiens YS-314.";
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
BMBL. APPOSEJ8: BACG18191.1;
SEQUENCE 180 AA: 19455 MW: EA6BFRCA54FCD761 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ġ
                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                       01-0EC-2001 (TrEMBLrel. 19, Created)
01-0EC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 29, Last sequence update)
Hypothetical protein acvB.
ACVB OR R01182 OR SMC00613.
ACVB OR R01182 OR SMC00613.
Bacteria; Proteobacteria Alphaproteobacteria; Rhizobianes; Rhizobiane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 21.2%; Score 7; DB 15; Length 194; Best Local Similarity 190.0%; Pred. No. 45; Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                       21.2%; Score 7; DB 16; Length 180; 100.0%; Pred. No. 42; ative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                     194 AA.
                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-1021;
MEDLINE-21396507; PubMed-11481430;
                                                                                                                                       Query Match
Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                   9 LGWLGAD 15
                                                                                                                                                                                       22 PALGLLK 28
                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=382;
                                                                                                                                                                                                                                                                     0920W4
                                                                                                                                                                                                                                          ò
   g
```

Search completed: September 26, 2003, 17:41:38 Job time : 20.1319 secs

113 LGWLGAD 119

```
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compagen .td
```

OM protein - protein search, using sw model

September 25, 2003, 17:28:58; Search time 102.289 Seconds (Without alignments) 313.452 Million cell updates/sec Run on:

202 1 PSGPSAPEAVTAKLVGVLWF.....TRLJRLSTINETFRKTQLYP 202 US-09-852-100A-2_COPY_68_269 Perfect score: Sequence:

1107863 seqs, 158726573 residues Searched:

Gapop 60.0 , Gapext 50.0

OLIGO

Scoring table:

0 Word size

1107863 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

1. SIDSI/gcgdatu/geneseq/qeneseqp.cmbl/AA1990.DAT:
2. SIDSI/gcgdatu/geneseq/qeneseqp.cmbl/AA1991.DAT:
3. SIDSI/gcgdatu/geneseqy-geneseqp.cmbl/AA1991.DAT:
4. SIDSI/gcgdatu/geneseqy-geneseqp.cmbl/AA1993.DAT:
5. SIDSI/gcgdatu/geneseqy-geneseqp.cmbl/AA1993.DAT:
6. SIDSI/gcgdatu/geneseqy-geneseqp.cmbl/AA1994.DAT:
7. SIDSI/gcgdatu/geneseqy-geneseqp.cmbl/AA1995.DAT:
8. SIDSI/gcgdatu/geneseqy-geneseqp.cmbl/AA1995.DAT:
8. SIDSI/gcgdatu/geneseqy-geneseqp.cmbl/AA1995.DAT:
9. SIDSI/gcgdatu/geneseqy-geneseqp.cmbl/AA1995.DAT:
11. SIDSI/gcgdatu/geneseqy-geneseqp-cmbl/AA1993.DAT:
12. SIDSI/gcgdatu/geneseqy-geneseqp-cmbl/AA1993.DAT:
13. SIDSI/gcgdatu/geneseqy-geneseqp-cmbl/AA1993.DAT:
14. SIDSI/gcgdatu/geneseqy-geneseqp-cmbl/AA1993.DAT:
15. SIDSI/gcgdatu/geneseqy-geneseqp-cmbl/AA1993.DAT:
16. SIDSI/gcgdatu/geneseqy-geneseqp-cmbl/AA1995.DAT:
17. SIDSI/gcgdatu/geneseqy-geneseqp-cmbl/AA1995.DAT:
18. SIDSI/gcgdatu/geneseqy-geneseqp-cmbl/AA1995.DAT:
19. SIDSI/gcgdatu/geneseqy-geneseqp-cmbl/AA1995.DAT:
19. SIDSI/gcgdatu/geneseqy-cmbl/AA1995.DAT:
19. SIDSI/gcgdatu/geneseqy-cmbl/AA1995.DAT:
20. SIDSI/gcgdatu/geneseqy-cmbl/AA1995.DAT:
21. SIDSI/gcgdatu/geneseqy-cmbl/AA1995.DAT:
22. SIDSI/gcgdatu/geneseqy-cmbl/AA1995.DAT:
23. SIDSI/gcgdatu/geneseqy-cmbl/AA1995.DAT:
24. SIDSI/gcgdatu/geneseqy-cmbl/AA1995.DAT:
25. SIDSI/gcgdatu/geneseqy-cmbl/AA1995.DAT:
26. SIDSI/gcgdatu/geneseqy-cmbl/AA1995.DAT:
27. SIDSI/gcgdatu/geneseqy-cmbl/AA1995.DAT:
28. SIDSI/gcgdatu/geneseqy-cmbl/AA1995.DAT:
28. SIDSI/gcgdatu/geneseqy-cmbl/AA1995.DAT:
29. SIDSI/gcgdatu/geneseqy-cmbl/AA1995.DAT:
20. SIDSI/gcgdatu/geneseqy-cmbl/AA1995. /SIDS1/gcqdata/geneseq/gcmesegp.embl/AA2001.UAT:*/SIDS1/gcqdata/geneseg/genesegp.embl/AA2002.DAT:*/SIDS1/gcgdata/geneseg/genesegp.embl/AA2003.DAT:* A_Geneseq_19Jun03:* 2222 2222 24:: 10: Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result boing printed, and is derived by analysis of the total score distribution.

			Description		Human beta-amyloid	Human beta-amyloid	Human BBP-1 prote:	Human 5' EST secre	Extrended human sec	Human 5' EST secre	RNA polymerase I:	Human BBP-1 protei	Human secreted pro
SOMMAKIES			CI		AAW94291	AAY70759	AAE33877	AAY12358	AAY36021	AAY12426	AAU97631	AAE33878	ABB11574
			DB		50	21	24	20	20	20	23	24	22
			e Match Length DB ID		269	269	569	139	162	148	100	89	225
	œ	Query	Match		100.0	100.0	100.0	65.8	55.0	40.6	21.3	8.4	4.5
			Score	1 - 1 - 1 - 1	202	202	202	133	111	82	43	17	6
		Result	ν. O		-	2	٣	4	Ś	و	7	80	σ

G.	Signal sequence ba	Cell penetrating p	Fluorescently labe	New peptide vector	Signal sequence ba	Signal-sequence-ba	nbəs 1	hila	Human beta-amyloid	_	Human Amyloid Apop	Humar gene 102 enc			human TANG	TANG	human TANG	human TANG	Orosophila melanog	X	G	RNA polymerase II	M. tuberculosis Rv	Leucine-rich repea	ě		Novel human diagno	Propionibacterium	Human ORFX protein	ibac	Protein of human s	ibac	M. tuberculosis Rv	Human secreted pro	Propionibacterium	
ABB776	<b>ABB</b> 811	ABG789	AAE236	ABB776	AAU783	ABG755	ABB825	ABB652	AAY707	ABR478	ABR484	ABR001	AAY276	AAB086	AAB086	AAB086	AAB086	AAB086	2 ABB55014	ABP629	ABB628	AAU976	<b>AA</b> U709	AAU752	AAM893	ABP085	ABG168	AAU6374	ABP0476	AAC5162	AA01444	-	AAU7095	AAG0164	AAU6095	
7	7	7 2	7 2	7 2	7 2	7 2	7 2	78 2	21 2	21 2	21 2	21 2	22 2	30 2	47 2	47 2	47 2	47 2	284 27	58 2	38 2	2	8	4 2	5 2	5	7 2	9	3 2	9	8	5 2	02 2	5 2	08 2	
8 4.0	4	4	4	4	4	4	4	4	<u>.</u>	4	-	4	4	4	4	7	4	7	0.4 8	-,*	4.0	٣.	ω.	œ.	œ.	ω.	3.	œ,	w.	m m	m m	w.	w.	m.	Э.	
3.0	.1	2.7	13	1.4	15	15	17	18	15	20	21	22	23	24	25	26	2.7	7.8	29	30	31	25	33	3.4	3.5	io m	3.7	38	36	04	4.1	42	4.3	44	4.5	

## AAW94291 standard; Protein; 269 AA

RESULT 1 AAW9429]

ALIGNMENTS

(first entry) 27-APR-1999 AAW94291;

Human beta-amyloid peptide-binding protein (3BP).

Seta-amyloid peptide binding protein, BBP, beta-amyloid protein, BAP, human, Alzheimer's disease.

Homo sapiens

Key

"specifically claimed fragment having beta-amyloid peptide binding activity" Location/Qualifiers 68..259 /note-W09846635-A2 22-CCT-1998. Region 

98WO-US07462. 97US-0064583. 14-APR-1998; 16-APR-1997;

(AMHP ) AMERICAN HOME PROD CORP.

Ozenberger BA; Jacobsen JS, Kajkowski EM, Bard JA, J Walker SG;

```
ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         õ
                                                                                                                     The present sequence represents a beta-amyloid peptide binding protein (BBP). The polynucleotide comprising the entire BBP nucleotide sequence of clone BBP1-f1 is deposited under the accession number ATCC 98617. The polynucleotide comprising a fragment of BBP (nucleotides 202-867 of the full length BBP) of clone pEK196 is deposited as ATCC 98399. Bost cells full length BBP) of clone pEK196 is deposited as ATCC 98399. Bost cells than stormed with a vector comprising the BBP nucleic acid are used for the recombinant production of the protein. The protein can be used for method for diagnosing a disease characterised by aberrant expression of human beta-amyloid protein (BAP). The protein can also be used in a method for screening for compounds which regulate expression of a BAP binding protein. The proteins, antibodies and identified compounds can be used in the treatment or prevention of Alzheimer's disease.
                                                                                                                                                                                                                                                                                                                                       ċ
                                                                                                                                                                                                                                                                                                                                                                                                                          121 ALSLFLGWLGADRFYLGYPALGLLKFCTVGFCGIGSLIDFILISMQ1VGPSDGSSYIIDY 183
                                                                                                                                                                                                                                                                                                                                                                                                             AIQEPVNCINYTAHVSCFPAPNITCKDSSGNEIHFIGNEVGFFKPISCRNVNGYSYKVAV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PSGPSAPEAVIARLVGVLWFVSVTTGPWGAVATSAGGERSLKCEDLKVGQYICKDPKIND 127
                                                                                                                                                                                                                                                                                                                                                             1 PSGPSAPEAVTARLVGVLWFVSVTTGPWGAVATSAGGEESLKGEDLKVGQYICKDPKIND 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1997.201
/label- DRF motif
/noter 'Substitution of the Arg abrogates protection"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Beta-amyloid peptide binding protein; BBP; BAP; tumour; suppresso;;
G-protein coupled receptor; GPCR; integral membrane protein; antiqen;
neuronal cell; nonhuman primate; NHP; G-protein signalling pathway;
apoptosis; immunogen; therapeutic; treatment; prevention; diagnostic.
                                                                                                                                                                                                                                                                                                                                        Gaps
                                               Polynucleotide encoding beta-amyloid peptide binding protein - used to identify inhibitors of beta-amyloid peptide for treating
                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                              DB 26; Length 269;
                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human beta-amyloid peptide (BAP) binding protein, 58Fl.
                                                                                                                                                                                                                                                                                                                                      ..
                                                                                                                                                                                                                                                                                                             100.0%; Score 202; DB 20
100.0%; Pred. No. 7e-193;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   213..238
/label- Transmembrane_domain_2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /label- Transmembrane_domain_l
                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 7; Pages 43-44; 59pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YGTRLIRLSIINETFRKTOLYP 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAX70759 standard; Protein; 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24-JUL-2000 (first entry)
                                                                                                                                                                                                                                                                                                                         Best Local Similarity 106.
Matches 202; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        177..198
                                                                        Alzheimer's disease
          WPI; 1999-086736/07
                                                                                                                                                                                                                                                                                     269 AA;
                       N-PSDB; AAX05735
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200022125-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                     89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY70759:
                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                             19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      248
                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Domain
                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY70759
P
                                                                                                                                                                                                                                                                                                                                                             õ
                                                                                                                                                                                                                                                                                                                                                                                     G
                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      a
```

```
The present sequence is the beta-amyloid peptide (BAP) binding protein-1 (BBP1). It is an integral membrane protein, that traverse the membrane butter. It is related to 6 protein-coupled receptor (GPCR) protein superfamily. It interacts with 6-alpha proteins and regulates the activity of G-protein signalling pathways. BBP genes are widely expressed in neurons. It functions as a suppressor of apoptosis induction. BBP proteins are used as immunogens to raise antibodies, useful as therapeutics and as antigens in solid phase assays. They are also useful as reagents to identify molecules which effect the interaction of BBP and a closed protein, that are useful in the treatment or prevention of diseases associated with apoptosis. The polynucleotides are useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 AIQEPVNCTNYTAHVSCFPAPNITCKDSSGNETHFTGNEVGFFKPISCHNVNGYSYKVAV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 ALSLFLGWIGADRFYLGYPALGLLKFCTVGFCGIGSLIDFILISMQIVGPSDGSSYIIDY 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Note: In claim 5, the patent claims an amino acid sequence from figure 2. However, figure 2 does not contain any sequence. It is inferred from the disclosure that the figure 2 sequence refers to BBP1 protein, shown in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ୍ଦ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; beta-amyloid peptide-binding protein; BAP; Abeta; betaAP; BBP;
Alzheimer's disease; AD; transgenic; transgenic animal; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                           Novel G-protein-coupled receptor-like proteins and polynucleotides useful for regulating apoptosis, comprises integral membrane protein traversing the membrane twice
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .
O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 269:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 202; DB 21
100.0%; Pred. No. 7e-193;
ivc 0; Mismatches 0
                                                                                                                                                                                                                                   .;
C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 1; Page 62-63; 68pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181 YGTRLTRLSITNETFRKTQLYP 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAE33877 standard; Protein; 269 AA.
                                                                                                                                                                                                                                   2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        248 YGTRLTRLSITNETFRKTÇLYP
                                                                                                                                                                         (AMHP ) AMERICAN HOME PROD CORP
                                                                                                                                                                                                                                   Ozenberger BA, Kajkowski EM,
                                                          99WO-US21621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   02-MAY-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         202; Conservative
                                                                                                                                                                                                                                                                                        WPI; 2000-317982/27.
N-PSDB; AA252369.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human BBP-1 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       269 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               this sequence.
                                                          13-0CT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             diagnostics.
20-APR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAE33877;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Malches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAE33877
ID AAE
```

27

Sat Sep

```
139 AA;
                                                                                                                                                                            N-PSDB; AAX41191
                                                                                                                        (GEST ) GENSET
             Home sapiens
                                 W09906548-A2
                                                                                                  01-AUG-1997;
                                                                             31-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13-SEP-1999
                                                        11-FEB-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY36C21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY 36021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3
                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                        68 PSGPSAPEAVTARLVGVLWFVSVTTGPWGAVATSAGGEESLKCEDLKVGQYICKDPKIND 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 AIQEPVNCTNYTAHVSCFPAPNIICKDSSGNETHFIGNEVGFFKPISCRNVNGYSYKVAV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ALSLFLGWLGADRFYLGYPALGLLKFCTVGFCGIGSLIDFILISMQIVGPSDGSSYIIDY 180
                                                                                                                                                                                                                                                                                                                                                                                                                                          1 PSGPSAPEAVTARLVGVLWFVSVTTGPWGAVATSAGGEESI,KCEDLKVGQY1CKDFKIND 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    forensic; gene therapy; chromosome mapping; signal peptide; upstream regulatory sequence; cytokine activity; cell proliferation: differentiation; hacmatopoiesis regulation; tissue growth regulation; reproductive hormome regulation; chemotactic; chemokinetic; hacmostatic; thrombolytic; anti-inflammatory; tumour inhibition
                                                                                                                                                                                                                                                                                               Abeta, betaAP)-binding (BBP) proteins and polynucleotides encoding such proteins. BBP sequences are useful to diagnose and/or treat discases associated with aberrant expression of human BAP such as Alzheimer's disease (AD). They are used to generate triansgenic animals. Sequences of the invention are also used in gene therapy. The present sequence
                                                                                                                                                                                                                                                                                      The present invention relates to novel human beta-amyloid peptide (BAP)
                                                                                                                                                                                                                     New human beta-amyloid peptide-binding protein, useful for diagnosing and/or treating diseases associated with aberrant expression of beta-amyloid peptide, e.g. Alzheimer's disease
                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                        Walker SG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; secreted protein; EST; expressed sequence tag; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 202; DB 24; Length 269; 100.0%; Pred. No. 7e-193;
                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                       Bard JA, Kajkowski EM, Jacobson JS,
                                                                                                                                                                                                                                                                                                                                                                                                                       .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     secreted protein SEQ ID NO:389.
                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181 YGTRLTRLSITNETFRKTQLYP 202
                                                                                                                                                                                                                                                                Claim 4; Page 84-85: 85pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY12358 standard; Protein; 139 AA
                                                                                       06-MAY-2002; 2002WO-US14223
                                                                                                           09-MAY-2001; 2001US-0852100
neuroprotective; nootropic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                      human BBP-1 protein.
                                                                                                                                                      Ozenberger BA, Bard J
Sofia HJ, Howland DS;
                                                                                                                                                                                      2003-120537/11
                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                           269 AA;
                                                                                                                                                                                                  N-PSDB; AAD51940
                                           W0200290459-A2
                                                                                                                                 (AMHP ) WYETH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human 5' EST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17-JUN-1999
                        Homo sapiens
                                                                 14-NOV-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                       202;
                                                                                                                                                                                                                                                                                                                                                                            Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY12358;
                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                            Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 4
  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  αd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                à
```

```
human secreted proteins, and encode the proteins given in ARV1250 to human secreted proteins, and encode the proteins given in ARV1250 to ARV12514, respectively. The proteins given the signal peptide and an N-terminal fragment of a secreted protein. The nuclein acid sequences can be used for develop products for diagnosis and therapy. They can also be used to develop products for diagnosis and therapy. The proteins obtained may have cytokine activity, cell proteins obtained may have cytokine activity, cell proliferation/differentiation activity, haemalopoiesis regulating activity, tissue growth regulating activity, reproductive hormone regulating activity, receptor/ligand activity, haemostatic and thrombolytic activity, receptor/ligand activity, anti-inflammatory activity, tumour inhibition activity or other activities. The products can be used in forensic, gene therapy and chromosome mapping promoter sequences can also be used for obtaining corresponding promoter activities the nucleic acides encoding the signal peptide can be used for directing extracellular secretion of a polypeptide into a membrane, or importing a polypeptide into a cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ü
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Secreted protein; human; cytokine; cellular proliferation; cell movement; cellular differentiation; immune system regulator; anti-inflammatory;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                62 IQEPVNCTNYTAHVSCFPAPNITCKDSSGNETHFTGNEVGFFKPISCRNVNGYSYKVAVA 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 SGPSAPEAVTARLVGVLWFVSVTTGPWGAVATSAGGEESLKCEDLKVGGYICKDPKINDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New rucleic acids encoding human secreted proteins—obtained freeDNA libraries prepared from e.g. liver, ovary, brain, prostate, kidney, lung, umbilical cord, placenta and colon tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Extended human secreted protein sequence, SEQ 1D NO. 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            65.8%; Score 133; DB 20; I ilarity 100.0%; Pred. No. 2.3e-124; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                          Duclert A, Dumas Milne Edwards J, Lacroix B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 27; Page 714-715; 824pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY35021 standard; Protein; 162 AA.
98WO-IB0:222.
                                                                                9708-6905135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          127 SEFEGWIGADE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         122 ISLFLGWLGADRF
                                                                                                                                                                                                                                                                                                                                  WPI: 1999-153776/13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
Matches 133; Conserv
```

```
This sequence is encoded by an extended human secreted protein coding sequence of the invention. The secreted proteins can be used in treating or controlling a variety of human conditions. The secreted proteins may act as sytokines or may affect cellular proliferation or differentiation or may act as immune system regulators, hemantopoinesis regulators. Itssue growth regulators of reproductive hormones or cell movement or have chemotactic/chemokinetic, receptor/ligand, anti-inflammatory or tumour inhibition activity. The DNAs can be used in forensic procedures to identify individuals or in diagnostic procedures to identify individuals or in diagnostic procedures to identify the breast procedures also useful for constructing a high resolution map of the fuman chiromosches. They can also be used for gene therapy to control or treat genetic diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6 APEAVTARLVGVLWFVSVTTGPWGAVATSAGGEESTKGEDLKVGQYICKDPKINDATGFP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11 APEAVTARLVGVLWEVSVTTGPWGAVAISAGGEESLKCEDLKVGÖYICKDPKINDÄTGEP 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human: secreted protein; EST; expressed sequence tag; diagnosis; forensic; gene therapy; chromosome mapping; signal peptide; upstream regulatory sequence; cytokine activity; cell proliferation; differentiation; haematopolesis regulation: tissue growth regulation; reproductive hormone regulation; chemokanic; chemokinetic; haemostatic; thrombolytic; anti-inflammatory; tumour inhibition.
                     reproductive hormone regulator; chemotaxis; chemokinesis; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Caps
 tumour inhibitor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                66 VNCTNYTAHVSCPPAPNITCKDSSGNETHFTGNEVGFFKPISCRNVNGYSY 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 71 VNCTNYTAHVSCFPAPNITCKDSSGNETHFTGNEVGFFFFPISCRNVNGYSY 12]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 162;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
haematopoiesis regulator; tissue growth regulator;
                                                                                                                                                                                                                                                                                                                                                    Bougueleret L, Duclert A, Dumas Milne Edwards J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             55.0%; Score 11%; DB 2%; 106.0%; Pred. No. 2.2e-102; iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human 5' EST secreted protein SEQ 1D NO:457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 9; Page 346-347; 516pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                          New isolated human secreted proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY12426 standard; Protein; 148 AA
                                                                                                                                                                                                                     98US-0096116.
97US-0069957.
98US-0074121.
98US-0081563.
                                                                                                                                                                                      98WO-IB02122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 55.0
Best Local Similarity 106.
Matches 111: Conservative
                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1999-385906/32.
N-PSDB; AAX97705.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            162 AA;
                                         genetic disease
                                                                                                                                                                                                                                                                                                                 (GEST ) GENSET
                                                                            Homo sapiens
                                                                                                           W09931236-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17-JUN-1999
                                                                                                                                                                                    17-DEC-1998;
                                                                                                                                                24-JUN-1999
                                                                                                                                                                                                                                                            09-FEB-1998;
                                                                                                                                                                                                                                                                              13-APR-1998;
                                                                                                                                                                                                                                         17-DEC-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 6
AAY12426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             qd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
```

```
AAX41094 to AAX41347 represent 5' expressed sequence tags (ESIs) for human secreted proteins, and encode the proteins given in AAY12261 to AAY12514, respectively. The proteins given represent the signal peptide and an N-terminal tragment of a secreted protein. The nucleic acid sequences can be used for producing secreted human gene products. They can also be used to develop products for diagnosis and therapy. The proliferation/differentiation activity, hammatopolesis regulating activity, tissue growth regulating activity, reproductive hormone regulating activity, chemotactic chemokinetic activity, hammatory activity, chemotactic chemokinetic activity, hammatory activity, tumour inhibition activity or other activities. The products
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      can be used in forensic, gene therapy and chromosome mapping procedures. The sequences can also be used for obtaining corresponding promoter sequences. The nucleic acids encoding the signal peptide can be used for directing extracellular secretion of a polypeptide or the insertion of a polypeptide into a membrane, or importing a polypeptide into a cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6 APEAVTARLVGVLWFVSVTTGPWGAVATSAGGEESLKGEDLKVGQYICKDPKINDATQEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                             - obtained from
                                                                                                                                                                                                                                                                                                         New nucleic acids encoding human secreted proteins - obtained freeDNA libraries prepared from e.g. liver, ovary, brain, prostato, kidney, lung, umbilical cord, placenta and colon tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  c:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 148;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             40.5%; Score 82; DB 20; Length 14:
100.0%; Pred. No. 1.7e-73;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RNA polymerase II subunit 11; cancer; HIV; infection;
                                                                                                                                                                                                                         Lacroix
                                                                                                                                                                                                                                                                                                                                                                               Claim 27; Page 763-764; 824pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RNA polymerase II subunit 11 protein.
                                                                                                                                                                                                                         Duclert A, Dumas Milne Edwards J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        71 VNCTNYTAHVSCEPAPNITCKD 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAU97631 standard; Protein; 100 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VNCTNYTAHVSCFPAPNITCKD 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         human immunodeficiency virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                40.58;
                                                                                                                    98WO-IB01222
                                                                                                                                                     97US-0905135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 100.
Matches 82; Conservative
                                                                                                                                                                                                                                                         WPI; 1999-153778/13.
N-PSDB; AAX41259.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               148 AA;
                                                                                                                                                                                        (GEST ) GENSET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unidentified
                                              WO9906548-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13-AUG-2002
                  Home sapiens
                                                                                                                    31-JUL-1998;
                                                                                                                                                     01-AUG-1997;
                                                                                 11 -FEB-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CN1331300-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAU97631
ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ð
```

65 7.0 us-09-852-100a-2_copy_68_269.rag

ő

Gaps

```
Human: cytokine; cell proliferation; cell differentiation; growth factor; haematopoiesis regulation; tissue growth; immunomodulator; activin; inhibin; chemotaxis; chemokinesis; thrombolysis; oncogenesis; proliferation; metastasis; cancer; tumour; haematopoietic disorder; myelcid cell disorder; hymphoid cell disorder; athmis athmis; athmis athmis; athmis; coronary heart disease; arterial ischaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Done disorder; osteoporosis; vascular growth disorder; tissue regeneration; wound healing; infection; immune disorder; cell culture; drug screening; gene therapy; antiinflammatory; antiasthmatic; antiarthritic; demostatic; antiarteriosclerotic; cytostatic; osteopathic; vasotropic; cardiant; virucide; antibacterial; antifungal; vulnerary; antiulcer.
                                                                                              The present invention relates to novel human beta-amyloid peptide (BAF: Abeta, betaAP)-binding (BBP) proteins and polynucleotides encoding such proteins. BBP sequences are useful to diagnose and/or treat diseases associated with aberrant expression of human BAP such as Alzheimer's disease (AD). They are used to generate transgenic animals. Sequence of the invention are also used in gene therapy. The present sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human proteins and DNA encoding sequences useful for preventing, treating or ameliorating a medical condition in a mammalian sub)ect
and/or treating diseases associated with aberrant expression of
                                                                                                                                                                                                                                                                                                                                        .;
O
                                                                                                                                                                                                                                                                                                Length 68;
                                                                                                                                                                                                                                                                                                                                        indels
                                                                                                                                                                                                                                                                                                DB 24; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human secreted protein homologue, SEO 1D NO:1944.
                    beta-amyloid peptide, e.g. Alzheimer's disease
                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                Score 17;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 20; Page 214; 1963pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABB11574 standard: peptide; 225 AA
                                                        Example 11; Fig 9; 85pp; English
                                                                                                                                                                                                                       is human BBP-1 protein fragment.
                                                                                                                                                                                                                                                                                                                                        .;
                                                                                                                                                                                                                                                                                                                                                                             150 GFCGIGSLIDFILLSMQ 166
                                                                                                                                                                                                                                                                                                                                                                                                    1 GPCGIGSLIDFILISMQ 17
                                                                                                                                                                                                                                                                                                  6.4%; ; ; 100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      03-FEB-2000; 2000US-0495914.
27-APR-2000; 2000US-0560875.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               05-FEB-2001; 2001WO-US03800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 e.g. arthritis and cancer
                                                                                                                                                                                                                                                                             Ouery Match
Best Local Similarity 100.0
Best Local 17, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-457746/45.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Liu C,
                                                                                                                                                                                                                                                             68 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; ABA08818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   W0200157188-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           09-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tang YT,
                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABB11574;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABB1157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Š
  a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ं
                                                                                                                                                                                                                                                                                                                                                                           This invention relates to the DNA and protein sequences of a novel polypeptide-RNA polymerase II subunit II protein. The invention also comprises a process for preparing the polypeptide of the invention by DNA recombination, the application of the polypeptide in treating diseases such as cancer, human immunodeficiency virus (HIV) infection, etc., the antagonist of the polypeptide and its medical action, and the application of the said polymotlectide are disciosed. The present sequence represents the RNA polymerase II subunit II protein of the
                                                                                                                                                                                                                                                                                 Polypeptide-RNA polymerase II subunit 1: and polynuclectide for coding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New human beta-amyloid peptide-binding protein, useful for diagnosing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human: bota-amyloid peptide-binding protein: BAP; Abeta: betaAP; BUP:
Alzheimer's disease: AD; transgenic; transgenic animal; gene therapy;
neuroprotective; nootropic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Walker SG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9 AVTARLVGVLWFVSVTTGPWGAVATSAGGEESLKCEDLKVGQY 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14 AVTARLVGVLWFVSVTTGPWGAVATSAGGEESLKCEDLKVGQY 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Jacobsen JS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21.3%; Score 43; DB 23; 1
100.0%; Pred. No. 8.6c-35;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kajkowski EM,
                                                                                                                                          (BODE-) BODE GENE DEV CO LTD SHANGHAI.
                                                                                                                                                                                                                                                                                                                                          Claim 1; Page 29; 32pp; Chinese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAE33878 standard; Protein; 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human BBP-1 protein fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        06-MAY-2002; 2002WO-US14223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              39-MAY-2001; 2001US-0852100
                                                          30-JUN-2000; 2000CN-0116963
                                                                                                  30-JUN-2000; 2000CN-0116963
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ozenberger BA, Bard J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2003-120537/11.
                                                                                                                                                                                                                       WPI; 2002-340664/38.
N-PSDB; ABK52558.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
Matches 43; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; AAD51978
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200290499-A2
                                                                                                                                                                                 Xic Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (AMHP ) WYETH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        02-MAY-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14-NOV-2002
                    16-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAE33878;
                                                                                                                                                                                 Mac Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAE33878
```

ò g 'n

```
name and possible regulatory activities; tissue growth activity; immunomodulatory activity; tissue growth activity; immunomodulatory activity; activities; heamostatic, thrombolic or chemokinetic activities; heamostatic, thrombolic or thrombolic or involved in oncogenesis, cancer cell proliferation or metastasis. Involved in oncogenesis, cancer cell proliferation or metastasis. Depending on their biological activities; polypeptides and nucleotides of the invention are useful for preventing, treating or ameliorating medical conditions, e.g., by protein or gene therapy. Such conditions include cancers, haematopoietic disorders of e.g., within or arthritis), proliferative retinopathy, atherosclerosis, coronary heart disease, proliferative retinopathy, atherosclerosis, coronary heart disease, proliferative retinopathy, atherosclerosis, coronary heart disease, proliferative retinopathy, atherosclerosis, costoporosis), and abnormal vascular growth. Polypeptides involved with tissue reqeneration and repair or nucleic acids encoding them.

The aling (e.g., of burns, incisions and ulcers), while those with immunomodulatory activities may be used in the treatment of viral, batcherial and fungal infections in addition to immune disorders.

Propertial and fungal infections in addition to immune disorders.

Propertial and fungal infections in addition to immune disorders.

Propertial and fungal infections in addition to immune disorders.
                      invention also relates to vectors and recombinant host cells comprising a nucleotide of the invention, methods of producing the nuvel polypeptides. and methods of detecting the nucleotides or polypeptides in a sample, and methods of identifying compounds which belief to polypeptides of the invention. Although sovel, many of the polypeptides of the invention have homolosy to known proteins, thereby giving an insight into their probable biological activities, and hence potential therapeutic applications. The polypeptides of the invention may bave various activities, including cytokine, cell proliferation or cell differentiation activities; stem cell growth factor activity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        that can be used to augment or replace cells damaged by liness, autoimmune disease or accidental damage. The polypoptides and nucleotides autoimmune disease or accidental damage. The polypoptides and nucleotides screening techniques. The present sequence represents a novel himan polypeptide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Intracellular delivery; transfection agent; cancer; infectious disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         rise to neuroepithelial cells
sequences ABA08225-ABA09574 represent nucleic acids encoding them. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Saps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      il growth. For example, such polypeptides may be used to
stem cells in culture to give rise to neuroepithelial of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .
O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gength 225;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4.5%; Score 9; D
.00.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABB77638 standard; peptide; 24 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4.5%,
100.0%; Pre
0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31-JUL-2000; 2000US-221932P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26-JUL-2001; 2001WO-US23406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (ACTI-) ACTIVE MOTIF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 100.
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  129 LGADRFYLG 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               176 LGADRFYIG 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New peptide vector#4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200210201-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    peptide vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               07-FEB-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         manipulate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABB77698;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABB77588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ŝ
```

```
The invention relates to a translection again, comparises a peptitude of a hydrophobic domain, a hydrophilic domain, optionally a spacer sequence between the domains and a functional group conjugated to at least one terminal of the peptide. Peptides of the invention are useful for a non-covalent association with and transport of a heterologous compound into a cell. They are also useful for promoting the callular compound into a cell. They are also useful for promoting the callular internalisation of at least one member e.g. peptide, proteins, antibodies, their derivatives and/or conjugates. They may form part of a pharmaceutical composition to deliver the compound selected from a cancer or an infectious disease, or which targets a cancerous cell or sa cancer or an infectious disease, or which targets a cancerous cell or pathogen-infected cell and to deliver a peptide or inhibitor that a scancer or an infectious disease, or which targets a cancerous cell of isrupts the activity of the enzyme. The agent of the invention has a transfection efficiency of at least 5% for at least two of the members of the group of the compounds and cell types, has a low foxicity, are assy to handle and casy to formulate in conjunction with the many different compound types that it can deliver. The peptides are serum sensitive, thus they bode particularly well for systemic and/or localised in patients. The current sequence represents a new amphipathic peptide control of the invention that contains a cationic nuclear localisation
                                                                                                             Transfection agent that comprises a peptide comprising hydrophobic and hydrophilic domain and having amino acid residues of specified length is useful for a non-covalent association with and transport of a heterologous compound into a cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                Archdeacon J;
                                                                                                                                                                                                                                                      The invention relates to a transfection agent comprises a peptide of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RBC; virus; vertebrate; therapeutic; tissue imaging;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ..
O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                Fernandez J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 8; DB 23
Pred. No. 1.7;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Signal sequence based peptide I MPS peptide.
                Heitz F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human immunodeficiency virus type 1. Rhesus macaque polyoma virus.
                                                                                                                                                                                                               Example 2; Page 61; 156pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABB81376 standard; peptide; 27 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Pr
                  Morris M, Mery J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-FEB-2001; 2001GB-0002561.
16-FEB-2001; 2001US-269528P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            yp41; memrane translocation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-FEB-2002; 2002WO-GB00437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Osery Match
Best Local Similarity Tub...
8, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           124 DFLGWLGA 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 LFLGWLGA 10
                                                                          WPI; 2002-329441/35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         blood cell:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200260416-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25-NCV-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   38-AUG-2002
                                       Horndorp K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABB81176;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sedneuce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KESULI 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Red
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABB81176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8
```

9

```
WPI: 2002-627577/67
             Wang R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAE23685
The invention relates to delivering an agent to a target site in a vertebrate. The method involves (a) loading a red blood cell RBD) with a virus or a virus-like particle (I) comprising an agent, (b) sensitizing RBC to render it more susceptible to disruption than unsensitized RBC; (c) introducing RBC into a vertebrate, and (d) applying energy to release (i). Steps (a) and (b) may be performed in any order. (II) (RBC loaded with a virus or a virus-like particle comprising a therapeutic agent) is useful for the delivery of a thorapeutic agent to a target site in a vertebrate, or in the preparation of a medicoment (or delivery of a therapeutic agent to a target site in a vertebrate. (II) is also useful to redivering one or more agents to a vertebrate and for treating or preventing a disease. The method is useful for delivering or in maging of tissues in vivo or ex vivo, preferably for preventing a disease. The method is useful for delivering an agent to a subcellular organic lessent sequence delivering an agent to a subcellular organic lessent sequence represents a signal sequence based peptide I MPS peptide, a chimera of the hydrophobic terminal domain of viral god1 protekn and the nuclear localisation signal (MLS) from the SV40 large actigen. This Iragment has
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0:
                                                                            Delivering agent to target site in vertebrate comprises loading red blood cell with virus or virus-like particle comprising agent, sensitizing cell, introducing cell into vertebrate and applying energy to release virus particle from cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Caps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cell penetrating peptide; cancer; tumour; melanomu; thymomu; lymphoma; sarcoma; lung cancer; non-fodgkin's lymphoma; leukaemid; Hodgkin's lymphoma; uterine cancer; cervical cancer; bladder cancer; kidney cancer; adenocarcinoma; breast cancer; prostate cancer; ovarian cancer; pancreatic cancer; vaccine; dendritic cancer; tumour infiltrating lymphocyte; TIL; human leukocyte antigen; HLA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           :
ن
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 23; Length 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cell penetrating peptide Signal-peptide II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Pred. No. 1.9
ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4.0%; Score 8;
                                                                                                                                                  Disclosure: Page 55; 87pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABG78990 standard; Peptide; 27 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (BAYU ) BAYLOR COLLEGE MEDICINE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-FEB-2001; 2001US-268687P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-FEB-2002; 2002WO-US05212.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 4.0
Best Local Similarity 100.
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       124 LFLGWLGA 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LFIGWLGA 10
                           Mchale AP, Craig R;
                                                    WPI; 2002-643355/69
(GEND-) GENDEL LID
                                                                                                                                                                                                                                                                                                                                                                                                                                                       27 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200264057-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-NOV-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22-AUG-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cytostatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABG78990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 12
ABG78990
```

```
the invention relates to a composition (i) comprising an immune effector cell and a cell penetrating peptide (CPP) associated with an antigen or antibody. Also included are (1) a vaccine comprising (1). CPP associated with an antigen, and a bharmaceutically acceptable carrier and (2) preparing a composition for a disease, by providing (I) antigen-associated with an antigen for disease, and introducing the antigens are, for example, tumour antigen netrs into the cell. The antigens are, for example, tumour antigen derived epitopes recognised by tumour infiltrating lymphocytes (TIL) of FLA (buman inmunity in an animal to a disease, by administering a mature dendritic munnity in an animal to a disease, by administering a mature dendritic cell comprising CPP associated with an antigen to disease, to the animal, such that following the administration, animal is protected from disease, where the animal comprises both CD4+ and CD8+ T cells. It is also useful for treating a disease (e.g. cancer, tumour, melanoma, thymoma, loukaemia, lymphoma, aarcoma, lung cancer, non-Hodgkin's lymphoma, icukaemia, uterine cancer, cervical cancer, bladder cancer, adenocarcinoma, breast cancer, brostate cancer, covarian cancer and pancreatic cancer, cervical cancer, breacher treatment including surgery, radiation, chemoticrapy or gene ticrapy. The administration of (I), preferably dendritic cell is prior to, subsequent to or concurrent with, the cancer treatment. The present cancer treatment including surgery radiation, clemoticrapy or gene ticrapy. The administration of (I), preferably dendritic cell is prior.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
Novel composition for treating a disease in an animal, comprises an immune effector cell and cell penetrating peptide associated with an antigen or antibody \cdot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RNA binding protein; mRNA quantification; gene expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fluorescently labelled RNA binding peptide #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match
4.0%; Score 8; DB 23;
best Local Similarity 100.0%; Pred. No. 1.9;
Matches 8; Conservative 0; Mismatches
                                                                                                                                                                                   Disclosure; Page 11; 61pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAE23685 standard; peptide; 27 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-SEP-2500; 2000US-236407P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28-SEP-2001; 2001WO-US30438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10-SEP-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             124 LFLGWLGA 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (CETT:-) CETTOWICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 LFLGWLGA 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI: 2002-452280/48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200227031-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unidentified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      04-APR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAE23685;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Busa WB;
```

```
ABB77687;
                   RESULT 14
                            Kev
                    A3B77687
                     ò
                  å
```

The present invention relates to a method of quantifying the expression of target genes in living cells. The method involves preciding cells than possess a target gene of interest which has been tagged with the binding site for an RNA binding protein and a fluorescently labelled RNA binding polypeptide that includes an RNA binding domain and calculating the guantity of target gene expression in the cells using fluorescence signalling techniques. The method is useful for quantifying expression of one or more target genes in living cells which comprise two or more distinct populations of cells. It is used to quantitate the expression Quantifying target gene expression in living cells that possess a target gene of interest tagged with the binding site for an RNA binding protein and fluorescently labeled RNA binding polypeptide including an of any target gene, including expression of protein-encoding messenger RNA genes, ribosomal RNA encoding genes and transfer RNA encoding genes so long as the RNA expression product from the target gene possesses a sequence or structure (the RNA tag) that is bound specifically by the RNA binding polypeptide being used. The present sequence is a fluorescently labelled RNA binding peptide. Claim 45; Page 44; 51pp; Engiish. RNA binding domain

27 AA; Sequence

Gaps :. ن DB 23; Length 27; . 1.9; 0; Indels 4.0%; Score 8; DB 2 100.0%; Pred. No. 1.9 Live 0; Mismatches Query Match
Best Local Similarity 100.
Matches 8: Conservative 124 LFLGWLGA 131 3 LFLGWLGA 10

ABB77687 standard; peptide; 27 AA.

01-JUL-2002 (first entry)

New peptide vector#3.

Intracellular delivery; transfection agent; cancer; infectious discase; peptide vector.

Synthetic

/note= "residue may be substituted with Phe" /note- "residue may be substituted with Ser" Location/Qualifiers Misc-difference 7 Misc-difference

WO200210201-A2

07-FEB-2002

26-JUL-2001; 2001WO-US23406

31-JUL-2000; 2000US-221932P. (ACTI-) ACTIVE MOTIF. (CNRS ) CENT NAT RECH SCI.

Ĺ Heitz J, Mery Morris M, Divida G, I Horndorp K;

Archdeacon

Fernandez č,

WPI; 2002-329441/36.

Transfection agent that comprises a peptide comprising hydrophobic and

(GEND-) GENDEL LID

Craig R;

01-FEB-2001; 16-FEB-2001;

```
The invention relates to a transfection agent comprises a peptide of about 16 - 30 amino acids in length. Peptides of the invention comparise a hydrophobic domain, a hydrophilic domain, optionally a spacer sequence between the domains and a functional group conjugated to at least one terminal of the peptide. Peptides of the invention are useful for a non-covalent association with and transport of a heterologous compound into a cell. They are also useful for prometing the cellular internalisation of at least one member e.g. peptide, proteins, antibodies, their derivatives and/or conjugates. They may form part of a pharmaceutical composition to deliver the compound, selected from a diagnostic or therapeutic compound, to treat at least one condition such as cancer or an infectious disease, or which targets a cancerous cell or pathogen-infected cell and to deliver a peptide or inhibitor that disrupts the activity of the enzyme. The agent of the invention has a transfection efficiency of at least 5% for at least two of the members of the name of the invention has a second of the invention of the invention has a second of the invention that the invention has a second of the invention that the invention tha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  :
:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the group of the compounds. The agent has a good delivery efficiency for a broad spectrum of compounds and cell types, has a low toxicity, are easy to handle and easy to formulate in conjunction with the many different compound types that it can deliver. The peptides are serum sensitive, thus they bode particularly well for systemic and/or localised in patients. The current sequence represents a new amphipathic peptide vector of the invention that contains a cationic nuclear localisation
hydrophilic domain and having amino acid residues of specified length
is useful for a non-covalent association with and transport of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Membrane translocation signal, signal sequence based peptide 1, red blood cell vehicle, polypeptide delivery, viral gp41 protein; simian virus 40; SV40; large antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4.0%; Score 8;
                                                                                                      Example 2; Page 61; 156pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ą
                                                       heterologous compound into a cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Pro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Signal sequence based peptide I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAU78348 standard; Peptide; 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2000WO-GB02848.
2000WO-GB03056.
2001WO-GB00417.
2001US-0785802.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rhesus macaque polyoma virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24-JUL-2001; 2001WO-GH03327.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18-JUN-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 100.
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 124 LFLGWLGA 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 LFLGWLGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  W020C207752-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24-JUL-2000;
09-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAU78348;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sedneuce.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sedneuce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 15
AAC78348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
```

```
The invention describes a method of preparing a red blood cell vehicle suitable for delivering an agent to a target site in a vertebrate comprising providing a red blood cell and loading the red blood cell with an agent-MTS (membrane translocation sequence) conjugate. The red blood cells produced may be used in the preparation of a medicament for delivery of an agent to or at a target site and of one or more agents to a vertebrate. The agent is actively released from the red blood cell vehicle by application of a stimulus to disrupt the red blood cell vehicle. This sequence represents signal sequence based peptide 1, a chimeric peptide of the hydrophobic terminal domain of the viral gp41 protein and the nuclear localisation signal iron simian virus 46 in the invention.
                                              Preparing a red blood cell vehicle suitable for delivering an agent to a target site in a vertebrate due to loading the red blood cell with an agent-membrane translocation sequence
                                                                                                                                                    Disclosure; Page 44; 135pp; English.
WPI; 2002-280593/32
```

27 AA; Sequence

Gaps Ġ Query Match

4.0%; Score 8; DB 23; Length 27;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 8; Conservative 0; Mismatches 0; Indels

Ċ

124 LFLGWLGA 131 1:111111 3 I.FLGWLGA 10

ò q Search completed: September 26, 2003, 17:39:24 Job time : 103.289 secs

```
) ORGANISM; Homo sapiens
US-09-411-628-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         138 YPALGLLK 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
  50000000000000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-222-938A-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-222-938A-13
                                                                                                                                                                                                                                                                                                                               JS-09-411-628-11
    TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH:
 ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               118. APP1

11. APP1

12. APP1

13. APP1

14. APP1

14. APP1

14. APP1

14. APP1

14. APP1

14. APP1

15. APP1

16. APP1

17. APP1

17. APP1

18. A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 11. Appl
Sequence 13, Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              . [dd¥
                                                                                                          (without alignments)
236.739 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                             September 26, 2003, 17:36:55; Search time 36:1021 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
Sequence
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence Sequence Sequence S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
Sequence
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
Sequence
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence Sequence Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sednence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sednence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                            .....TRLTELSITIBLEFRKTQLYF
                                                                                                                                                                                                                                                                                                                                                                                                          /cgn2_6/ptodata/1/iaa/5A_COXH.pep:*
/cgn2_6/ptodata/1/iaa/5B_COXH.pep:*
/cgn2_6/ptodata/1/iaa/6A_COXH.pep:*
/cgn2_6/ptodata/1/iaa/6B_COXH.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COXH.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COXH.pep:*
              GenCore version 5.1.6
Copyright (c) 1993 - 2603 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -09-222-938A-13
-09-252-991A-21850
-09-134-001C-5239
                                                                                                                                                                                                                                                                                               fotal number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-467-527A-:
US-08-467-528-3
                                                                                                                                                                                                                                             328717 seqs, 42310858 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUMMARIES
                                                                                                                                                  US-09-852-100A-2_COPY_68_269
                                                                                                                                                                                                                                                                                                                                                                   Post-processing: Listing first 45 summaries
                                                                   protein search, using sw model
                                                                                                                                                              202
1 PSGPSAPEAVTARLVGVLWF....
                                                                                                                                                                                                     OLIGO
Gapop 60.0 , Gapext 60.0
                                                                                                                                                                                                                                                                                                                                                                                                Issued_Paterts_AA:*
                                                                                                                                                                                                                                                                                                                              length: 0
length: 200000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               358
1183
1183
2004
2013
462
462
643
673
673
767
767
767
767
767
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query
Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mirimum DB seq
Maximum DB seq
                                                                                                                                                 Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score
                                                                                                                                                                                                      Scoring table:
                                                                                                                                                                                                                                                                        Word size :
                                                                   OM protein
                                                                                                                                                                                                                                                                                                                                                                                                Database :
                                                                                                                                                                           Sequence:
                                                                                                                                                                                                                                            Searched:
                                                                                              Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Result
No.
```

```
Ċ
                                                                                                                                                               Appli
       sequence 238. As Sequence 314. As Sequence 311. As Sequence 1. App Sequence 2. App Sequence 6. App Sequence 2. App Sequence 2. App Sequence 2. App Sequence 2. App Sequence 6. App Sequence 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               seguence 6,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ·,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEREMAL INFORMATION:
SEREMAL INFORMATION:
TITLE OF INVENTION: COND. GENOMIC, AND PREDICTED PROTEIN
TITLE OF INVENTION: SECURES OF LEARNING-INCUCED KINASES
FILE REFERENCE: 13751-707
CURRENT APPLICATION NUMBER: US/09/411,628
CURRENT APPLICATION NUMBER: US/09/411,628
CURRENT FILING DATE: 1999-10-01
EARLIER APPLICATION NUMBER: US 60/102,906
SARLIER FILING DATE: 1999-10-02
NUMBER OF SEQ ID NOS: 16
SOFTWARE: FASISED for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 13. Application US/0922938A
Parcht No. 643108
Sequence No. 643108
Sequence No. 643108
Sequence No. 643108
Sequence No. 643108
APPLICANT: Volument, Philip
APPLICANT: Murphy, Christopher
APPLICANT: Murphy, Christopher
APPLICANT: Guzman, Luz-Maria
TITLE OF INVENTION: ESSENTIAL BACTERIAL GENES AND THEIR USE
FILE REFERENCE: 07334/060001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 358;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
US-09-205-258-298
US-08-905-223-314
US-09-248-947-306
US-09-248-947-306
US-09-228-742A-11
US-08-75-508-2
US-08-75-508-2
US-09-251-835-2
US-09-251-835-2
US-09-251-835-2
US-09-251-835-2
US-09-251-835-2
US-09-251-835-2
US-09-261-835-6
US-09-38-261A-5
US-09-08-261A-6
US-09-68-609-6
US-09-68-808-609-6
US-09-68-808-609-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ore 8; DB 4;
red. No. 5.5;
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/222,938A CURRENT FILING DATE: 1998-12-30 NUMBER OF SEQ ID NOS: 102 SCFTWARE: FastSEQ for Mindows Version 3.0 SEQ ID NO 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 8; I
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 11, Application US/09411628 Patent No. 6428994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRI
ORGANISM: Streptococcus pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4.0%; So
ilarity 100.0%; P
Conservative 0;
```

ò ΩĢ

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .;
O
                                                                          GENERAL INFORMATION:
APPLICANT: FILZ, Christian
APPLICANT: Youngman, Philip
TITLE OF INVENTION: USE OF YNES, ESSENTIAL BACTERIAL GENES AND POLYPEPTICES
FILE REFERENCE: 06286-69001
CURRENT APPLICATION NUMBER: US/69/163,445B
CURRENT APPLICATION NUMBER: US/69/163,445B
CURRENT APPLICATION NUMBER: US/69/163,445B
PRIOR APPLICATION NUMBER: US/69/163,465B
PRIOR FILING DATE: 1997-12-31
NUMBER OF SEQ ID NOS: 12
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 1
LENGTH: 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TILE OF INVENTION: SF, a No. 6558910el Family of Taste Receptors FILE REFERENCE: 02307E-039600US
CURRENT APPLICATION NUMBER: US/09/393,634
CURRENT PLING DATE: 1959-09-10
NUMBER OF SRO IC NOS: 92
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ..
O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FOLLOWING TOWARD TOWARD THE STANDARD TOWARD 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 213;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 245;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0: Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 3.5%; Score 7; DB 4 Best Local Similarity 100.0%; Pred. No. 34; Matches 7; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3.5%; Score 7; E
100.0%; Pred. No.
tive 0; Mismatch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         any amino acid
                     // Sequence 1, Application US/09163445B
// Patent No. 6472377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            : URGANISM: Streptococcus pneumoniae
US-09-163-445B-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 55, Application US/09393634
; Patent No. 6558910
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; sequence 56, Application US/09393634
; Patent No. 6558910
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: human GR11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cucry Match
Best Local Similarity Tuc..
The 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: MOD_RES
LOCATION: (1)..(245)
CTHER INFORMATION: Xaa
US-09-393-634-55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      105 AVATSAG 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                156 SLIDFIL 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30 AVATSAG 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Adler, JG
APPLICANT: KYba, Nich
APPLICANT: Myba, Nich
APPLICANT: Hoon, Mar)
APPLICANT: The Regen
APPLICANT: The Regen
APPLICANT: The Regen
APPLICANT: S repress
APPLICANT: OP INVENTION:
TILE REFERENCE: 02307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               42 SLIDFIL 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER ... SOFTWARE: Pate
SECID NO 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 6
US-09-393-634-55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-393-634-56
US-03-163-445B-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      d:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INCORPATION:
APPLICANT: Lynn Dougette-Stamm et al
APPLICANT: Lynn Dougette-Stamm et al
TITLE OF INVENTION: WOLLETC ACID AND AMING ACID SEQUENCES RELATING TO STAPHYLOGOGUS
TITLE OF INVENTION: EPIDERALDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GIC-007
CURRENT APPLICATION NUMBER: US/09/7134,001C
CURRENT APPLICATION NUMBER: US 60/054,964
PRIOR FILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-11-08
NUMBER OF SEQ ID NOS: 5674
                                                                                                                                                                                                                                                                                                                                                                                                 FEGUREAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TG PSEUDOMONAS:
TITLE OF INVENTION: ARENGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: ARENGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252.991A
CURRENT FILING DATE: 1999-02-18
PRIOR FILING DATE: 1999-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 21850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ċ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ġ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Scips
                                                                                       Saps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                   .
ت
                        Length 114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 183:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 204;
                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indeis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3.5%; Score 7; DB 4; 100.0%; Pred. No. 33; ative 0; Mismatches
                           DB 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3.5%; Score 7; DB 4;
100.0%; Pred. No. 29;
rative 6; Mismatches
                     3.5%; Score 7; DB 4
100.0%; Pred. No. 19;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                US-09-252-991A-21850
; Sequence 21850, Application US/0925299:A
; Patent No. 6551795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Application US/09134601C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7 ORGANISM: Staphylococcus epidermidis
US-09-134-001C-5239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; ORGANISM: Pseudomonas aeruginosa US-09-252-991A-21850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                    Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30 AVATSAG 36
                                                                                                                                                                              30 AVATSAG 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 PSGPSAP 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Patent No. 6380370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-134-001C-5239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 5239,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO 5239
                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
```

ò

å

RESULT, 5

q

ò

<u>:</u>:

Gaps

.. O

```
Sequence 29267, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: MAIC J. Rubenfield et al.
TILLE OF INVENTION: AEKGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILLE REPRENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT APPLICATION NUMBER: US/09/252,991A
PRIOR APPLICATION NUMBER: US/09/252,991A
PRIOR APPLICATION NUMBER: US/09/252,991A
PRIOR FILING DATE: 1998-02-18
PRIOR PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
: LENGTH: 483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 617;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 483;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                   Length 462
                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Hodge, Martin
FITLE OF INVENTION: No. 6558903el Kinases and Uses Thereof
FILE REFERENCE: 35600/183781
CURRENT APPLICATION NUMBER: US/09/345,473E
CURRENT FILING DATE: 1999-06-30
NUMBER OF SEQ ID NOS: 62
SOFIWARE: FASTSEO for Mindows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3.5%; Score 7; DB 4;
100.0%; Pred. No. 71;
ative 0; Mismatches
                                                                                                                                                                                     DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0.ery Match 3.5%; Score 7; DB 4, Bost Local Similarity 100.0%; Pred. No. 89; Matches 7; Conservative 0; Mismatches
                                                                                                                                                                                 3.5%; Score 7; DB 4
100.0%; Pred. No. 68;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              . Sequence 44, Application US/09345473E : Patent No. 6558903
                                                                                             ; TYPE: PKT
: ORGANISM: Acinetobacter baumannii
US-09-328-352-6888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Pseudomonas acruginosa
    CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 6888
                                                                                                                                                                Query Match
Best Local Similarity 100.0
Feet 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ouery Match
Best Local Similarity 100.00
Feet Tools 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                   139 PALGLLK 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   438 PALGLIK 444
                                                                                                                                                                                                                                                                         121 ALSLFLG 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 ALSLFLG 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            582 ALSLFLG 588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                     RESULT 10
US-09-252-991A-29267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-252-991A-29267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 11
US-09-345-473E-44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-345-473E-44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 44
                                                                          LENGIH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH:
                                                                                                                                                                                                                                                                            ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GD
D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 6888, Application US/09328352
Patent No. 5562958
Patent No. 5562958
Patent No. 5562958
TITLE OF INVENTION: APPLICANT GARY L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RECATING TO ACINETOBACIER TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ë
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0
                APPLICANT: Zuker, Charles S.
APPLICANT: Adler, Jon Elliot
APPLICANT: Ryba, Nick
APPLICANT: Ryba, Nick
APPLICANT: Mucler, Ken
APPLICANT: Hoon Mark
APPLICANT: Hoon Mark
APPLICANT: The Regents of the University o: Calliornia
APPLICANT: The Gevernment of the University of the
APPLICANT: The Gevernment of the University of the
APPLICANT: as represented by the Secretary of the
APPLICANT: OF PRESENCE: C2307F-C980001CS
CURRENT APPLICATION NUMBER: CS/C9/393,634
CURRENT FILING DATE: 1999-09-10
NUMBER OF SEQ ID NOS: 92
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 56
LENGTH: 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Science
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3.5%: Score 7; DB 4; Length 451;
100.0%; Pred. No. 67;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Hodge, Martin
TITLE OF INVENTION: No. 6558903e1 Kinases and Uses Thereof
FILE REPERENCE: 35800/18378:
CURRENT APPLICATION NUMBER: US/C9/345,473F.
CURRENT APPLICATION NUMBER: US/C9/345,473F.
NUMBER OF SEQ ID NOS: 62
SOFTWARE: SESTSEQ for Windows Version: 4.0
SEQ ID NO 455
LENGTH: 451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C; Indeis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DE 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3.5%; Score 7; DB 4
100.0%; Pred. No. 48;
tive 6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: human GR12
NAME/KEY: MOD_RES
COATION: (1)..(315)
OTHER INFORMATION: Xaa = any amino acid
US-09-393-634-56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 45, Application US/09345473E
Patent No. 6558903
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7: Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IYPE: PRT ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 156 SLIDFIL 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 ALSIFLG 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   416 ALSLFLG 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1111111
42 SLIDFIL 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 7: Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-328-352-6888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 8
US-09-345-473E-45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-345-473E-45
                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Op
O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           δ
```

ò

Gaps

·.

Gaps

.. O

```
PRICK ALLING DATE: 1998-06-04
PRICK FILING DATE: 1998-06-04
PRICK APPLICATION NUMBER: 60/088029
PRICK APPLICATION NUMBER: 60/08803
PRICK APPLICATION NUMBER: 60/088030
PRICK APPLICATION NUMBER: 60/088033
PRICK PILING DATE: 1998-06-04
PRICK FILING DATE: 1998-06-04
PRICK PLING DATE: 1998-06-04
PRICK PLING DATE: 1998-06-04
PRICK PLING DATE: 1998-06-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: 60/088212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 60/088217
                                                    Godowski,Paul J.
Grimaldi,J.Christopher
Gurney,Austin L.
                                                                                                                                                                                                                                                Watanabe, Colin K.
Williams, P. Mickey
Wood, William I.
                                                                                                                                                                                                           Stewart, Timothy A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1998-06-05
                                                                                                                                                                                           Roy, Margaret Ann
                                                                                                                                                  Pan, James
Paoni, Nicholas F.
                Gerritsen, Mary E.
Gerber, Hanspeter
                                                                                                             Kljavin, Ivar J.
                                    Goddará, Audrey
                                                                                                                              Napier, Mary A.
                                                                                                                                                                                                                           Daniel
                                                                                                                                                                                                                               Tumas,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR
                                                        Sequence 26617, Application US/09252991A

Patent No. 655195

GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TILLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSHROWENS
TILLE OF INVENTION: AERUGINOSA FOR DIASNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT PILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 26617
LENGTH: 643
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ن
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2, Application US/09063950C
Patent No. 6225085
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: HOLIZMAN, DOUGLAS A.
TITLE OF INVENTION: THEREFOR
FILLE REFERENCE: HOLION
CURRENT APPLICATION UNDER: US/09/063,950C
CURRENT FILING DATE: 1998-04-21
NUMBER OF SEQ ID NOS: 9
SEQ ID NO 2
LENGTH: 673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Seps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ő
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 643;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 673;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0: Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 3.5%; Sco. 100.0%; Pred. No. ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 7; DB 3; Pred, No. 96; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 14
US-09-996-243-52
Sequence 52, Application US/09996243
Patent No. 6478825
                                                                                                                                                                                                                                                                                                                                                                                                        : Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3.5%; ;
100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: AShkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Bolstein, David
APPLICANT: Bosnoyers.Licc
APPLICANT: Eaton, Dan I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9.5
Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fong, Sherman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OKGANISM: Homo sapiens
US-09-063-950-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 7; Conservat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            190 ITNETFR 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 GPSAPEA 9
                                                      US-09-252-991A-26617
                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-252-991A-26617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 13
US-09-063-950-2
                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
```

```
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
                                                                                                             TILLE OF LIVENING DATE: 200.—11.14

CURRENT APPLICATION NUMBER: US/09/996,243

CURRENT FILING DATE: 200.—11.14

PRICE PELLING DATE: 200.—11.14

PRICE PLING DATE: 1997-66-16

PRIOR APPLICATION NUMBER: 60/06250

PRIOR PELLING DATE: 1997-10-17

PRIOR APPLICATION NUMBER: 60/065186

PRIOR PELLING DATE: 1997-11-13

PRIOR PELLING DATE: 1997-11-12

PRIOR APPLICATION NUMBER: 60/065311

PRIOR PELLING DATE: 1997-11-24

PRIOR APPLICATION NUMBER: 60/06570

PRIOR PELLING DATE: 1997-11-24

PRIOR PELLING DATE: 1998-02-25

PRIOR APPLICATION NUMBER: 60/08312

PRIOR APPLICATION NUMBER: 60/08700

PRIOR PELLING DATE: 1998-06-02

PRIOR PELLING DATE: 1998-06-02

PRIOR PELLING DATE: 1998-06-02

PRIOR APPLICATION NUMBER: 60/088025

PRIOR PELLING DATE: 1998-06-04

PRIOR PELLING DATE: 1998-06-04

PRIOR PELLING DATE: 1998-06-04

PRIOR PELLING DATE: 1998-06-04

PRIOR PELLING DATE: 1998-06-07

PRIOR PELLING DATE: 1998-06-07
```

us-09-852-100a-2_copy_68_269.rai

S

```
R FILING DATE: 1998-06-18
R APPLICATION NUMBER: 60/089908
R APPLICATION NUMBER: 60/089947
R PILING DATE: 1998-06-19
R APPLICATION NUMBER: 60/089948
R FILING DATE: 1998-06-19
R APPLICATION NUMBER: 60/08952
R FILING DATE: 1998-06-19
R RILING DATE: 1998-06-19
R PILING DATE: 1998-06-18
R FILING DATE: 1998-06-18
R FILING DATE: 1998-06-18
R FILING DATE: 1998-06-28
R FILING DATE: 1998-06-28
R FILING DATE: 1998-06-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R FILING DATE: 1998-06-17
R APPLICATION NUMBER: 60/065538
R PELING DATE: 1998-06-17
R APPLICATION NUMBER: 60/089598
R FILING DATE: 1996-06-17
R APPLICATION NUMBER: 60/089599
R FILING DATE: 1996-06-17
R APPLICATION NUMBER: 60/089600
R FILING DATE: 1998-06-17
R APPLICATION NUMBER: 60/089607
R APPLICATION NUMBER: 60/089607
R APPLICATION NUMBER: 60/089538
R FILING DATE: 1998-06-17
                                                                                                                                                                                            R FILING DATE: 1998-06-10

R FILING DATE: 1998-06-10

R FILING DATE: 1998-06-10

R APPLICATION NUMBER: 60/088826

R APPLICATION NUMBER: 60/088888

R APPLICATION NUMBER: 60/088888

R APPLICATION NUMBER: 60/088888
                                                                                                                                  APPLICATION NIMBER: 60/083742
FILING DATE: 1998-06-10
APPLICATION NUMBER: 60/088810
FILING DATE: 1998-06-10
                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 60/089105
FILING DATE: 1998-06-12
APPLICATION NUMBER: 60/089405
FILING DATE: 1998-06-16
APPLICATION NUMBER: 60/089512
FILING DATE: 1998-06-05
APPLICATION NUMBER: 60/088655
FILING DATE: 1998-06-09
APPLICATION NUMBER: 60/088734
FILING DATE: 1998-06-10
                                                                             FILING DATE: 1998-06-10
APPLICATION NUMBER: 60/088738
FILING DATE: 1998-06-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 1998-06-22
APPLICATION NUMBER: 60/090349
FILING DATE: 1998-06-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 62/090355
FILING DATE: 1998-06-23
APPLICATION NUMBER: 60/090429
FILING DATE: 1998-06-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 1998-06-24
APPLICATION NUMBER: 60/090435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 60/090444
FILING DATE: 1998-06-24
APPLICATION NUMBER: 60/090445
FILING DATE: 1998-06-24
                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 60/08861
FILING DATE: 1998-06-11
APPLICATION NUMBER: 60/088676
FILING DATE: 1998-06-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 1998-06-16
APPLICATION NUMBER: 60/089514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 1998-06-16
APPLICATION NUMBER: 60/089532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: 60/08980:
FILING DAFE: 1998-06-18
APPLICATION NUMBER: 60/089907
FILING DATE: 1998-06-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 60/090431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LING DATE: 1998-06-24
                                                               PRIOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR
PRIOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR
PRIOR
PRIOR
PRIOR
PRIOR
PRIOR
PRIOR
PRIOR
PRIOR
PRIOR
PRIOR
PRIOR
PRIOR
PRIOR
```

PRIOR APPLICATION NUMBER: 60, 24 PRIOR FILING DATE: 1998-06-24 PRIOR FILING DATE: 1998-06-24 PRIOR PRIOR DATE: 1998-06-24 PRIOR PRIOR DATE: 1998-06-24 PRIOR FILING DATE: 1998-06-24 PRIOR FILING DATE: 1998-06-24 PRIOR FILING DATE: 1998-06-25 PRIOR FILING DATE: 1998-07-02 PRIOR FILING DATE: 1998-07-03 PRIOR PRIOR PRIOR DATE: 1998-07-03 PRIOR PRIOR PRIOR DATE: 1998-07-03 PRIOR PRIOR PRIOR DATE: 1998-07-07 PRIOR PRIO
--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------

...

```
September 26, 2003, 17:41:48; Search time 70.485; Seconds (without alignments) 433.624 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                    ..TRLIRLS!INETFRKTQLYP 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     runisheu_Application=_Ann.

2. cgn2_6/ptodata/2/pubpaa/US07_PUHCOMR.pep:*

2. cgn2_6/ptodata/2/pubpaa/US07_PUHCOMR.pep:*

3. cgn2_6/ptodata/2/pubpaa/US07_NEW_UBD.pep:*

3. cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*

5. cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*

6. cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*

7. cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*

8. cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*

9. cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*

11: cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*

12: cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*

13: cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*

14: cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*

15: cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*

16: cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*

17: cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*

18: cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*

18: cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*

18: cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                566894 seqs, 151307093 residues
                                                                                                                                                                                                                                                                                       US-09-852-100A-2_COPY_68_259
202
I PSGPSAPEAVTARLV3VLWF......
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Published_Applications_AA:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Post-processing: Listing first 45 summaries
                                                                                                                   · protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                           OLIGO
Gapop 60.0 , Gapext 60.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10::
112::
14::
15::
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0
                                                                                                                                                                                                                                                                                          Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                           Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Word size :
                                                                                                                   OM protein
                                                                                                                                                                                                                                                                                                                                                    Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Database
                                                                                                                                                                          Run on:
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Sescription	Sequence 2, Appl3	Sequence 2, Appli	Sequence 2, Appli	Sequence 288, App	Sequence 305, App	Sequence 28, Appl		Sequence 2, Appl:	27.	8	Sequence 6, April	82.	82.	230,	82, ;
SCMMARIES	Q.:	US-09-852-100A-2	US-09-833-503A-2	US-10-199-881-2	US-10-226-956-288	US-10-211-088-306	US-09-915-914B-28	US-09-785-802A-8	US-09-965-876A-2	US-09-915-914B-27	US-10-077-555-8	US-09-833-503A-6	US-09-992-600A-82	US-09-924-340-62	US-09-974-879-230	US-09-992-095B-82
	53	6	10	15	15	15	11	10	7.7	::	5	CE	7.7	11	11	13
	% Query Match Length DB	269	269	569	21	21	24	27	27	27	27	221	221	221	221	221
	% Query Match	100.0	100.0	100.0	0.4	4.0	4.0	4.0	4.0	4.0	4 · C	<) •••	0.4	<b>7</b>	4.0	4.0
	Score	202	202	202	80	8	80	œ	89	œ	ထ	Ø	œ	യ	œ	8
	Result No.	н	2	3	4	Ŋ	9	7	8	6	10	11	12	13	14	15

154-678-82 Sequence 82, 999-570-82 Sequence 82, 0000-489-82 Sequence 82, 0000-986-82 Sequence 82, 199-881-6	305-736-230 Sequence 230, 796-753-50 Sequence 50, 796-753-48 Sequence 48, 794-794-11 Sequence 11, 154-251-13 Sequence 13, 67-550-80 Sequence 80, 1	32. Sequence 332. Sequence 332	006-8108-332 015-858-332 015-858-332 012-1218-332 006-1178-332 017-5278-332 017-5278-332 013-4368-332 011-6718-332	OBSTRUCT
12 US-10 12 US-09 15 US-10 15 US-10 15 US-10	1 US-09 1 US-09 2 US-10 5 US-10 5 US-10	1 US-09 2 US-10 2 US-10 2 US-10 2 US-10 2 US-10	,0000000000	TIA
22222	222 230 247 358 114	177 177 177 177 188 188 188 188 188 188	14444444444444444444444444444444444444	
44444			, സ.	
သောလာထားက ေ	8888877	<i>~~~~~~~</i>		
16 118 119 220	222 223 224 254 26	2000 E 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	. Რ Რ Რ Რ Რ Რ Რ Რ Რ Რ Რ Რ Რ Რ Რ Რ Რ Რ Რ	

## ALIGNMENTS

```
Sequence 2, Application US/09852100A
Sequence 2, Application US/09852100A
Sequence 2, Application US/09852200A
Sequence 2, Application US/098525A1
General No. US200200585A2A
GENERAL INFORMATION:
APPLICANT American Enne Products
TILLE OF INVENTION Beta amyloid Peptide-Binding Proteins and Polynucleotides En. TILLE OF INVENTION Beta amyloid Peptide-Binding Proteins and Polynucleotides En. TILLE OF INVENTION Same
FILE REFERENCE: AAPPS126A2
CURRET APPLICATION NUMBER: US 09/172,590
PRIOR FILING DATE: 1999-10-13
PRIOR RELING DATE: 1999-10-13
PRIOR FILING DATE: 1999-00-15
PRIOR FILING DATE: 1999-00-13
PRIO
```

61 ATQEPVNCTNYTAHVSCFPAPNITCKDSSGNETHFTGNEVGFFKPISCRNVKGYSYKVAV 120

6

5

ô

qq

5

```
::
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                      68 PSGPSAPEAVTARLVGVLWFVSVTTGPWGAVATSAGGEESLKCEDLKVGGYICKDPKIND 127
                                                                                                                                                                                                                                                                                                                                                                                                    61 ATQEPVNCTNYTAHVSCFPAPNITCKDSSGNETHFTGNEVGFFKPISCRNVNGYSYKVAV 126
                                                                                                                                                                                                                                                                                                                                                                                                                           128 AIQEPVNCINYTAHVSCFPAPNITCKDSSGNETHFTGNEVGFFKPISCRNVNGYSYKVAV 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21 ALSLFLGWLGADRFYLGYPALGLLKFCTVGFCGIGSLIDFILISMQIVGPSDGSSYIIDY 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 PSGPSAPEAVTARLVGVLWFVSVTTGPWGAVATSAGGEESLKCEDLKVGQYICKDPKIND 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Brophy, Colleen
APPLICANT: Komalavilas, Padmini
APPLICANT: Komalavilas, Padmini
APPLICANT: Panith, Alyssa
APPLICANT: Seal, Bandon L.
APPLICANT: Seal, Brandon L.
TILLE OF INVENTION: REAGENTS AND METHODS FOR SMOOTH MUSCLE THERAPLES
FILE REFERENCE: ASU-1061-US
                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                          Length 269;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 21;
                                                                                                                                                                                                                                                                      indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                            DB 15;
                                                                                                                                                                                                                                                                        .
                                                                                                                                                                                                                                                 2e-190;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                          100.0%; Score 202;
100.0%; Pred. No. 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/10/226,956
CURRENT FILING DAIE: 2002-08-23
FRIOR APPLICATION NUMBER: 60/314,535
PRIOR FILING DATE: 2001-08-23
NUMBER OF SEQ ID NOS: 320
SCFTWARE: PALENTIN version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Grery Match 4.0%; Score 8; D Best Local Similarity 100.0%; Pred. No. Matches 8; Conservative 0; Mismatch
  PRIOR APPLICATION NUMBER: US 60/104,104 PRIOR FILING DATE: 1996-10-13 NUMBER OF SEQ ID NOS: 45 SOFTWARE PATENTIN VERSION 3.1 SEQ ID NO 2 LENGTH: 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            181 YGTRLIRLSIINETFRKIQLYP 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   248 YGTRLTRLSITNETFRKIQLYP 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: Synthetic peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 306, Application US/10211088 | Fublication No. US2003010447941 | GENERAL INFORMATION: APPLICANT: Bright, Gary R. APPLICANT: Premkumar, D. David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 288, Application US/10226956 Publication No. US20030060399A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                     : TYPE: PRI
CRGANISM: Homo sapiens
US-10-199-881-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  124 LFLGWLGA 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 LFLGWLGA 10
                                                                                                                                                                                                                                                 Local Similarity
nes 202; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 5
US-10-211-088-306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-10-225-956-288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-226-956-288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NC 288
LENGTH: 21
                                                                                                                                                                                                                            Cuery Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE
                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                      ä
                                                                                                                                                                                                                                                                                                                                                                                                                                             30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                â
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2
                                                                                                                                                                                                                                                                                                                                                                                                         ŝ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ŝ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5
                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Grenberger, Bradley A
APPLICANT: Kajkowski, Elleen M
APPLICANT: Kajkowski, Elleen M
APPLICANT: Lo, Ching-Hestung F
APPLICANT: American Hong F
APPLICANT: American Hong F
APPLICANT: American Hong F
APPLICANT: American Hong Collaboration
IITLE OF INVENTION: Polynuclectides Encoded By Them, and Methods of Using
TITLE OF INVENTION: Same
FILE REFERENCE: AHP98165-00PCI
CURRENT PAPPLICATION NUMBER: US/09/833,503A
CURRENT FILING DATE: 2000-10-13
PRIOR FILING DATE: 1998-10-13
PRIOR FILING DATE: 1998-10-13
SEQ ID NOS: 6
SUFFMANER: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2, Application US/10199881
Publication No. US20030096356A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Wyeth

ITLE OF INVENTION: Encoded by Them, and Methods of Using Same"

ITLE OF INVENTION: Encoded by Them, and Methods of Using Same"

ITLE REFERENCE: AHP98165C1
CURRENT APPLICATION NUMBER: US/10/199,881
CURRENT FILING DATE: 2002-07-18
PRIOR PPLICATION NUMBER: PCT/ US99/21621
PRIOR FILING DATE: 1999-10-13
PRIOR FILING DATE: 1999-10-13
PRIOR FILING DATE: 2001-12-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ċ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12) ALSLFIGWLGADRFYIGYPALGLLKFCTVGFCGIGSLIDFILISMOIVGPSDGSSYIIDY 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 ATQEPVNCTNYTAHVSCFPAPNITCKDSSGNETHFTGNEVGFFKPISCRNVNGYSYKVAV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 ALSLFLGWEGADRFYLGYPALGLLKFCTVGFGGIGSLIBFILLSMQIVBPSDGSSYIIDY :#?
                                                                                         1 PSGPSAPEAVTARLVGVLWFVSVTTGPWGAVATSAGGEESLKCEDLKVGQYICKDFKIND 60
Saps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ..
O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 269;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 202; DB 10; 100.0%; Pred. No. 2e-190;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181 YGTRLTRESITNETFRKTOLY? 202
                                                                                                                                                          181 YGTRLIRLSITNETFRKTQLYP 202
                                                                                                                                                                                                     248 YGTRLIRLSIINETFRKTQLYP 259
                                                                                                                                                                                                                                                                                                          Sequence 2, Application US/09833503A Patent No. US20020146760Al
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             202; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-833-503A-2
                                                                                                                                                                                                                                                                                        US-09-833-503A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 3
US-10-199-881-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
```

ò g ò q οž d οy

```
APPLICANT: Callomics, Inc.
APPLICANT: Busa, William B
TITLE OF INVENTION: Methods and Reagents for Live-cell Gene Expression Ocantifica
FILE REPERENCE: 00-789-A
CURRENT APPLICATION NUMBER: US/09/965,876A
CURRENT APPLICATION NUMBER: US 60/236,407
PRIOR FILING DATE: 2001-09-28
PRIOR FILING DATE: 2000-09-28
NUMBER OF SEQ ID NOS: 42
SEQ ID NO 2
LENGTH: 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: HORDGOP, Kyle
TITLE OF INVENTION: PEPTIDE-MEDIATED DELIVERY OF MOLECULES INTO CELLS
FILE REFERENCE: AM-00105. P. 1.1
CURRENT APPLICATION NUMBER: 02/09/915,914B
PRIOR APPLICATION DATE: 2001-07-26
PRIOR APPLICATION NUMBER: US 60/221,932
PRIOR FILING DATE: 2000-07-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ..
                                                                                                                                                                                                                                                                                                                                     0:
                                                                                                                                                                                                                                                                                       Query Match 4.0%; Score 8; DB 10; Length 27; Best Local Similarity 100.0%; Pred. No. 1.3; Matches 8; Conservative 0; Mismatches 0; Indeis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ouery Match
4.0%; Score 8; UB 31; Length 27;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 8; Conservative 0; Mismatches 0; Indels
CURRENT APPLICATION NUMBER: US/09/785,802A
CURRENT FILING DATE: 2001-02-16
PRIOR APPLICATION NUMBER: US 09/748,06
PRIOR APPLICATION NUMBER: US 09/748,789
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
NUMBER OF SEQ ID NOS: 16
SOFTWARE: Patentin version 3.1
SECTION 12 7
                                                                                                                                                                                                                               ORGANISM: Human immunodeficiency virus
US-C9-785-802A-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: Synthetic peptide US-09-965-876A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 27, Application US/09915914B Publication No. US26030119725A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2, Application US/09965876A Publication No. US20030096243A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IYPE: PRT
ORGANISM: ARTIFICIAL SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Fernandez, Joseph
APPLICANT: Hellz, Frederic
APPLICANT: MOTIS, MAY
APPLICANT: Mery, Jean
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Archdeacon, John APPLICANT: Horndorp, Kyle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Divita, Gilles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           124 LFLGWLGA 131
                                                                                                                                                                                                                                                                                                                                                                            124 LFLGWLGA 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1111111
3 LFLGWLGA 10
                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 9
US-09-915-9143-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 8
US-09-965-876A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2
                                                                                                                                                                                                                                                                                                                                                                                5
                                                                                                                                                                                                                                                                                                                                                                                                                   ä
                 TITLE OF INVENTION, NO. US20030104479Alel Fusion Proteins And Assays For Molecular Bi File Reperence: 01-1022-US CURRENT APPLICATION UNMBER: 05/10/211,088 CURRENT FILING DATE: 2002-10-15 PRIOR APPLICATION NUMBER: 60/309,395 PRIOR FILING DATE: 2001-08-01 PRIOR FILING DATE: 2001-08-01 PRIOR FILING DATE: 2001-12-13 NUMBER OF SEQ ID NOS: 366 SOFTWARE: Patentin version 3.1 SEQ ID NO 306 LENGTH: 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ٥
                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Saps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 8, Application US/09785802A
Patent No. US20020151004A1
GENERAL INFORMATION:
TITLE OF INVENTION: DELIVERY VEHICLES AND METHODS FOR USING THE SAME
FILE REFERENCE: 11067/2035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3
                                                                                                                                                                                                                                                                                                                                                                                                                                          ..
O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4.0%; Score 8; DB 11; Length 24; 106.0%; Pred. No. 1.2; Uive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                 Length 21:
                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: Protein-derived transport peptide US-10-211-088-306
                                                                                                                                                                                                                                                                                                                                                                                               DB 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                               Query Match
4.0%; Score 8; i
Best Local Similarity 100.0%; Pred. No.
Matches 8; Conservative 0; Mismatch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: Synthetic sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-915-914B-28
Sequence 28, Application US/099:5914B
Publication No. US20030119725A1
FUBLICATION NO. WARPING:
APPLICANT: Divita, Gilles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                        TYPE: PRT ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 100.
Matches 8; Conservative
Chen, Yih-Tai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    124 LFLGWLGA 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             124 LFLGWLGA 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11111111
3 LFLGWLGA 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 LFLGWLGA 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-915-914B-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-785-802A-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
    APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         дd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
```

:.

```
::
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                   Gaps
                                                                                 <u>ن</u>
                                                                                                                                                                                                                                                                                                                                    APPLICANI: DELAKA, HICAKI
TILLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF
FILE REPERBNEE: 91.034.31V
CURRENT APPLICATION UNBER: US/09/992,600A
CURRENT FILING DATE: 2001-11-13
FRICA PPLICATION NUMBER: US/09/924,340
PRIOR FILING DATE: 2001-08-06
PRIOR FILING DATE: 2001-08-06
PRIOR FILING DATE: 2001-08-06
PRIOR FILING DATE: 2001-08-06
PRIOR APPLICATION NUMBER: US 60/302,277
PRIOR APPLICATION NUMBER: US 60/302,277
PRIOR APPLICATION NUMBER: US 60/208,698
PRIOR APPLICATION NUMBER: US 60/298,698
PRIOR PELING DATE: 2001-06-15
PRIOR FILING DATE: 2001-06-25
NUMBER OF SEQ ID NOS: 114
SOFTWARE JPALENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Bejanin, Stephane
APPLICANT: Tanaka, Hiroaki
ITLE OF INVENTION: HUMA CDNAS AND PROTEINS AND USES THEREOF
FILE REFERENCE: 91.052.REG
CURRENT APPLICATION HUMBER: US/09/924,340
CURRENT APPLICATION NUMBER: US/09/924,346
FRIOR APPLICATION NUMBER: US/09/924,346
FRIOR PILING DATE: 2001-06-05
FRIOR FILING DATE: 2001-06-29
FRIOR FILING DATE: 2001-06-29
FRIOR APPLICATION NUMBER: US/05/293,698
FRIOR APPLICATION NUMBER: US/05/293,698
FRIOR APPLICATION NUMBER: US/06-15
FRIOR APPLICATION NUMBER: US/06-15
FRIOR PILING DATE: 2001-06-15
FRIOR APPLICATION NUMBER: US/05-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 221;
                                     4.0%; Score 8; DB 16; Length 221.
106.0%; Pred. No. 9.2;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4.0%; Score 8; DB 1
100.0%; Pred, No. 9.2
iive 0; Mismatches
                                                                                                                                                                                                                                                          Sequence 82, Application US/09992600A Publication No. US2030027161A1 Publication No. US2030027161A1 APPLICANT: Benjanin, Stephane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 82, Application US/09924340 Publication No. US20630027248A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Overy Match
Best Local Similarity 100...
Fest Local 8; Conservative
                                         Owery Match
Best Local Similarity 106.
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 130 GADREYIG 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        130 GADRFYLG 137
                                                                                                                                              . NAME/KEY: SIGNAL
.: LOCATION: 1..32
US-09-992-600A-82
                                                                                                                                                                                                                       RESULT 12
US-09-992-500A-82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-924-340-82
    US-08-833-203A-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ŝ
                                                                                                                           3
                                                                                                                                                            £
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 8, Application US/10077555
Publication No. US20030077289A1
CREERAL INFORMATION:
CREERAL INFORMATION:
CREERAL INFORMATION:
CONTRIBUTION: Use of Cell-Penetrating Peptides to Generate Antitumor Immunity
FILE REFERENCE: P02373051/10200806
CURRENT PILING DATE: 2002-02-15
PRIOR APPLICATION NUMBER: US 60/268,687
PRIOR FILING DATE: 2001-02-15
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              S
                                                                                                                                                                                                                                            ÷.
                                                                                                                                                                                                                                            Gales
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                          6
                                                                                                                                                                                                  DB 11; Length 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 27,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C: Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    58 15;
3. 1.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4.0%; Score 8; DB 1
100.0%; Pred. No. 1.3
tive 0; Mismatches
                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                  4.0%; Score 8; L
1.00.0%; Pred. No.
tive 0; Mismatch
                                                                                                                                       ; OTHER INFORMATION: Synthetic sequence US-09-915-9148-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: Synthetic Peptide US-10-077-555-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: 60/104,164 PRIOR FILING DATE: 1998-10-13 NUMBER OF SEQ ID NOS: 6 SOFTWARE: PATENTIN VET: 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 6, Application US/09833503A Patent No. US20020146760A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT ORGANISM: Artificial Sequence
                    SOFTWARE: PatentIn version 3.1
SEQ ID NO 27
                                                                                                    ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100.
Matches 8; Conservative
                                                                                                                                                                                                                     Best Local Similarity 100.
Matches 8; Conservative
NUMBER OF SEQ ID NOS: 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   124 LFLGWLGA 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                               124 LFLGWLGA 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 LFLGWLGA 10
                                                                                                                                                                                                                                                                                                           3 SFLGWEGA 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-833-503A-6
                                                                                                                                                                                                                                                                                                                                                                                                       US-10-077-555-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 8
LENGTH: 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 6
                                                                                                                                                                                                      Query Match
                                                                                                                       FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       qc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
```

ċ,

Gaps

..

```
: DOCATION: (184); CTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids 3S-08-574-879-230
                                                                                                                                                Ouery Match

4.0%; Score 8; DB 11; Length 221;
Best Local Similarity 100.0%; Pred. No. 9.2;
Natches 8; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4.0%; Score 8;
100.0%; Pred. No
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cuery Match
Best Local Similarity 1900.
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                    TYPE: PRT ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              130 GADRFYLG 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     130 GADRFYLG 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; LOCATION: 1..32
US-09-992-095B-82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: JPat
SHQ ID NO 82
LENGTH: 221
                                                                                                                                                                                                                                                                                                                                                                                                        ë
                                                                                                                                                                                                                                                                                                                                                                                                           ć
                                                                                                                                                                                                                                                                                                                                        Query Match
4.0%; Score 8; DB 11; Length 221;
Best Local Similarity 100.0%; Pred. No. 9.2;
Matches 8; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PAPLICATE: Rosen et al.

TITLE OF INVENTION: 125 Human Secreted Proteins
FILE REFERENCE: P2020P2
CURRENT APPLICATION NUMBER: US/09/974,879
CURRENT FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: US 60/239,893
PRIOR APPLICATION NUMBER: US 60/239,893
PRIOR PILING DATE: 2000-10-13
PRIOR APPLICATION NUMBER: US 69/818,683
PRIOR APPLICATION NUMBER: US 69/818,683
PRIOR APPLICATION NUMBER: PCT/US9#/23435
PRIOR APPLICATION NUMBER: PCT/US9#/23435
PRIOR APPLICATION NUMBER: US 60/664,911
PRIOR FILING DATE: 1998-11-04
PRIOR PILING DATE: 1998-11-04
PRIOR FILING DATE: 1998-11-05
PRIOR PRILING DATE: 1998-11-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR FILING UNIE: 1977-11-07
PRIOR FILING CATE: 1977-11-07
PRIOR APPLICATION NUMBER: 0.S 60/064,912
PRIOR APPLICATION NUMBER: 0.S 60/064,912
PRIOR APPLICATION NUMBER: 0.S 60/064,913
PRIOR FILING DATE: 1997-11-07
PRIOR PRILICATION NUMBER: 0.S 60/064,987
PRIOR FILING DATE: 1997-11-07
PRIOR FILING DATE: 1997-11-07
PRIOR FILING DATE: 1997-11-07
PRIOR PRILING DATE: 1997-11-07
PRIOR PLING DATE: 1997-11-07
PRIOR PLING DATE: 1997-11-07
PRIOR FILING DATE: 1997-11-07
PRIOR PLING DATE: 1997-11-17
PRIOR FILING DATE: 1997-11-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 14
US-09-974-879-230
US-09-974-879-230
Separation US/09974879
Publication No. US20030028603A1
GENERAL INFORMATION:
NUMBER OF SEQ ID NOS: 112
SOFTWARE: JPatent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRI
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        174 GADRFYLG 181
                                                                                                                                                          ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     130 GADRFYLG 137
                                                                                                                                                                                                                       NAME/KEY: SIGNAL
                                                                                                                                                                                                                                                    ; LOCATION: 1..32
US-09-924-340-82
                                                             SEQ ID NO 82
LENGTH: 221
                                                                                                                             TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
```

```
Gaps
RESULT 15
US-09-092-095B-82
Sequence 82, Application US/09992095B
FOURTAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Benjamin, Stephane
APPLICANT: Tanaka, Hicaki,
ITILE OF INVENTION: HUMAN CENAS AND PROTEINS AND USES THEREOF
TILLE REFERENCE: 91.US5.D1V
CURRENT APPLICATION NUMBER: US/09/992,095B
CURRENT APPLICATION NUMBER: US/09/992,095B
FRIOR APPLICATION NUMBER: US 60/924,340
FRIOR APPLICATION NUMBER: PCT/IB01/01715
FRIOR FILING DATE: 2001-08-36
FRIOR FILING DATE: 2001-08-36
FRIOR FILING DATE: 2001-08-36
FRIOR FILING DATE: 2001-08-36
FRIOR APPLICATION NUMBER: US 60/305,456
FRIOR FILING DATE: 2001-08-36
FRIOR APPLICATION NUMBER: US 60/305,277
FRIOR APPLICATION NUMBER: US 60/298,698
FRIOR FILING DATE: 2001-06-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         UB 12; Length 221; . 9.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. 9.2
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Search completed: September 26, 2003, 17:55:12 Job time: 71.4851 secs
```

```
GenCore version 5.1.6
Copyright (c) 1993 - 2063 Compuges Ltd.
```

OM protein - protein search, using sw model

Run on:

202 1 PSGPSAPEAVTARLVGVLWF.....TRLTRLSITNETFRKTGLYP 202 US-09-852-100A-2_COPY_68_259 Title: Perfect score:

Scoring table: Sequence:

OLIGO Gapop 60.0 , Gapext 50.0

283308 seqs, 95168682 residues Searched:

283308 total number of hits satisfying chosen parameters:

0

Word size :

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

PIR_76:*
1: pirl:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

	200 and 200 an	mercal control	protein kinase (EC	serine/threching p	hypothetical profe		Ca]	2.	acetyl transferase	etic	inorganic pyrophos		hypothetical prote	conserved hypothet	B. subtilis YneS p	conserved hypothet		conserved hypothet	conserved hypothet		conserved hypothet	C	probable oxoacyl (	probable sugar ABC	conserved hypothet	hypothetical prote	hypotherical prote	ica;	probable 3'(2'),5'	probable ABC trans	trans-sulfuration
	Ę	4 !	S 2	S227	T160	T287	B975	H7		T48	67.	D64	T2015	AB159	AD1			B86	C950	C97	690	3755	F7.1	C7136	D701	T22:2	A71237	B725	B8173	AB01	GB106
	10:01 10:01																			213 2											
фD	Query	יים רכזו ד	3·*	0· <b>*</b>		4 · C	3.5	3.5												3.5				•					•		•
	0,00	2000	<b>x</b>	œ	æ	80	7	7	۲-	7	۲	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7
	Resuit		1	7	m	4	Š	9	7	œ	O	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27		53

Alintrons: 152/3; 170/3 Cisuperfamily: kinase-related transforming protein; protein kinase homology Ciseywords: AFP; phosphotransferase; serine/threonine-specific protein kinase Fig.3-296/Domain: protein kinase homology <KINN F:11-19/Region: protein kinase AFP-binding motif

Length 376;

4.0%; Score 8; DB 2;

Query Match

Sering/threonine protein kinase KKIALKE (EC 2.7.1.-) - human cispecies: Homo sapiens (man) cispecies: Homo sapiens (man) cispecies: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 19-Dec-1997 Ciscession, A.L. submitted to the EMBL Data Library, May 1992 Air Greence number: S22743 Air Greence number: S22743 Air Greence number: S22745 Air Satus: preliminary Air May 1992 Air Satus: preliminary Air Satus: Bresidues: 1-376 CMEY> Air Sesidues: 1-376 CMEY> Air Sesidues: 1-376 CMEY> Air Sesidues: EMBL: X66359 Cispectics: Air Satus: EMBL: X66359 Cispectics: Air Satus: EMBL: X66359 Cispectics: Air Satus Sat

probable MFS trans probable para-amic ubiquinol-cytochrc hypotherical protein LiM kinase (EC 2.7) probable pabB proteapsular polysacch NADH2 dehydrogenas probable xanthine hypotherical protein hypotherical protecolicin B - Escher probable RRP19-11k NA(+)-1inked D-alamyo-inositol trans hypothetical prote	st him st	ore 8; DB 2; Length 358; red. No. 3.2; Mismatches 0; Indels 0; Gaps 0;
415 2 C83544 418 2 D86936 419 1 J00346 442 2 B75634 451 1 JE0240 456 2 T44650 495 2 A95984 495 2 A95984 510 2 T12819 510 2 T12819 540 2 C84744 547 2 T43605 543 2 T25690	ALIGNMENTS  7) cdc2-related KKIALRE  40.  80.  80.  80.  80.  80.  80.  80.	0.00°.
	ALI 523.83 protein kinase (EC 2.7.1.37) cdc2-related control of the case of the case of the cort. 1994 *sequence_revision of the case of	Similarity 8: Conservat YPALGLLK 145           YPALGLLK 260
0 00 00 00 00 00 00 00 00 00 00 00 00 0	RESULT 1 \$23383 protein kin C.Species: C.Species: C.Species: C.Accession EMBO U 11, A.M. Reference A.S. Reference C.S. Superference C.S. Superference C.S. Reference C.S. R	Query Match Bost Local Matches Cy 138

Ë

```
probable PE protein - Mycobacterium tuberculosis (strain H37KV)

Species: Mycobacterium tuberculosis

C;Species: Mycobacterium tuberculosis

C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999

C;Accession: H70898

R;Cole, S. I.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordc

C;Accession: H70898

R;Deville, R.; Paville, R.; Feltwell, T.; Gentles, S.; Hamiln, N.; Folroyc

Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Hamiln, N.; Folroyc

Rajandream, M.A.; Rogers, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.

A;Authors: Sqares, R.; Salston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.

A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete gen A;Reference number: A70809: MUID:98295987; PMID:9634230

A;Accession: H70898

A;Accession: H70898

A;Accession: H70898

A;Residues: 1-102 <COL>
A;Cross-references: GB:280108; GB:All23456; NID:q3256012; PIDN:CAB02191.1; PII:e2655

A;Experimental source: strain H37RV
                        Riccodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Ourollo, B.; Goic A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Mirkelz, Science 294, 2323-2329, 2020.
Asiance 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A:Cross-references: GB:AJ248284; GB:AL096836; NID:95457730; PIDN:CAB49323.1; PID:el5
A:Experimental source: strain Orsay
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 K:anonymous, Genoscope
s:imhited to the EMBL Data Library, July 1999
A:Description: Pyrococcus abyssi genome sequence: insights into archaeal chrom:some
A:Reference number: A75001
                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: GB:AE007869; PIDN:AAK87547.1; PID:q15156883; GSPDB:GN00169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C.Species: Pyrococcus abyssi
C.Date: 26-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Aug-1999
C.Accession: D75155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    :
O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 102,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        acetyl transferase PAB2081 - Pyrococcus abyssi (strain Crsay)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .
( )
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3.5%; Score 7; DB 2;
100.0%; Pred. No. 12;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3.5%; Score 7; DB 2
160.0%; Pred. No. 11;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A: Map position: circular chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9.5%
Bost Local Similarity 160.6
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Sest Local Similarity 160.
Matches 7: Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8 EAVTARL 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8 EAVTARL 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18 EAVTARL 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A.Status: preliminary
A.Molecule type: DNA
A.Residues: 1-141 <KAW>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Accession: D75155
C;Accession: B97574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C:Genetics:
A:Gene: AGR_C_3268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Gene: PAB2081
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C: Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT ?
D75155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ć
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pypothetical protein F16H11.5 - Caenorhabditis elegans (Species: Caenorhabditis elegans C) Species: Caenorhabditis elegans (Species: Caenorhabditis elegans (Species: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_charge 18-Fcb-2000 (Sacession: T16082 #sequence of C. Species: 20-Sep-1999 #species: 20-Sep-1999 #sp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hypothetical protein AGR_C_3268 [imported] - Agrobacterium tumefaciens (strain CS8. Cord
C.Species: Agrobacterium tumefaciens
C.bate: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 18-Nov-2662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A:Map position: 1
A:Introns: 53/2: 81/3: 117/1: 256/3: 274/2: 357/3: 443/2: 485/3: 544/3: 585/3: 637/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A:Status: preliminary; translated from GB/EMBL/UDBJ
A:Rolecule type: DNA
A:Residues: 1-73 <GRA.
A:Residues: 1-73 <GRA.
A:Cross-references: EMBL-AF003740; PIDN:AAC48141.1; GSPUH:GNG0019; CESP:041011.
A:Experimental source: strain Bristol N2; clone C41011
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypothetical protein C41D11.5 - Caenorhabditis clequ:s
C:Species: Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 29-Oct-1999 *sequence_revision 29-Oct-1999 *text_change 29-Oct-1599
C:Accession: T.Maggi, L.
S:Chaccession: T.Maggi, L.
S:Daftung, S.; Maggi, L.
A:Bescription: The sequence of C. elegans cosmid C41D11.
A:Reference number: 220522
A:Reference number: 220522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sdaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Map position: X
A;Introns: 71/1: 93/1: 187/3: 281/3: 316/3: 420/2: 460/1: 513/3: 545/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ċ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 548;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 753
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
                                                      Indels
                                                      ċ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4.0%; Score 8; DB 2;
100.0%; Pred. No. 4.6;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4.0%; Score 8; DB 2; 100.0%; Pred. No. 6.1;
    Pred. No. 3.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                      Mismatches
                                                      0
100.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 100.
Matches 8; Conservative
                                                      8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               130 GADRFYLG 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      [111111]
GADREYLG 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            109 KDSSGNET 116
                                                                                                                                           138 YPALGLLK 145
                                                                                                                                                                                                       86 KDSSGNET 93
    Rest Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Gene: CESP:C41D11.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C; Genetics
                                                 Matches
```

õ

ن

g ò

: :

```
PETOND, J.F.; White, O.; Keriavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fielscimann, Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, P.; Moterson, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Fatthey Nature 388, 539-547, 1997

A.Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser A.Reference number: Active genome sequence of the gastric pathogen Helicobacter pylori. A.Reference number: Active genome sequence of the gastric pathogen Helicobacter pylori. A.Reference number: Active genome sequence of the gastric pathogen Helicobacter pylori. A.Recession: D64597
A.Recession: D64597
A.Status: preliminary; nucleic acid sequence not shown; translation not shown A.Roicoule type: DNA
A.Residues: 1-73 < TONA
A.Cross-references: GB:AE000576; GB:AE000511; NID:g2313736; PIDN:AAD07684.1; FID:g2: C.; Superfamily: inorganic pyrophosphatase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A.Map position: 5
A.Introns: 33/1: 77/1: 103/3: 128/1
C.Superfamily: LR11 protein: laminin-type EGF-like homology: LDL receptor ligand-bir
F:37-74/Domain: LDL receptor ligand-binding repeat homology <LDL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            conserved hypothetical protein, B. subtilis YneS protein homolog lin1323 [imported] C.Species: Listeria innocua C.Species: Lastria innocua C.Date: 27-Nov-2001 *sequence_revision 27-Nov-2001 *text_change 14-Dec-2001 C.Accession: AB1598
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Accession: T2958
A: Reference number: 219230
A: Accession: T20157
A: Status: pre-liminary; translated from GB/EMBL/DD65
A: Status: pre-liminary; translated from GB/EMBL/DD65
A: Status: pre-liminary; translated from GB/EMBL/DD65
A: Most decences: EMBL: 275012; PIDN: CAB01419.1; GSPDB: GN00023; CESP: F58H1.7
A: Cross references: EMBL: 275012; PIDN: CAB01419.1; GSPDB: GN00023; CESP: F58H1.7
A: Gross references: EMBL: 275012; DIDN: CAB01419.1; GSPDB: GN00023; CESP: F58H1.7
A: Residues: pre-liminary; translated from GB/EMBL/DD83
A: Status: pre-liminary; translated from GB/EMBL/DD83
A: Most decide type: DNA
A: Residues: 1-185 < WI2>
A: Cross-references: EMBL: 275954; PIDN: CAB00110.1; GSPDB: GN00023; CESP: F58H1.7
A: Status: pre-liminary decided from GB/EMBL/DD83
A: Status: pre-liminary decided from GB/EMBL/DD83
A: Most decided from GB/EMBL/DD83
A: Status: pre-liminary decided from GB/EMBL/DD83
A: Most decided from G
inorganic pyrophosphatase - Helicobacter pylori (strain 26695)
C.Species: Helicobacter pylori
C.Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 22-Jun-1999
C.Accession: D64597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hypothetical protein F58H1.7 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: i5-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 23-Sep-2002
C:Accession: T20157; T22958
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 3.5%; Score 7; DB 2; Length 173; Best Local Similarity 100.0%; Pred. No. 19; Matches 7; Conservative 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 3.5%; Score 7; DB 2; Length 185:
Best Local Similarity 100.0%; Pred. No. 20;
Matches 7; Conservative 0; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   117 KVAVALS 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 KVAVALS 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12 ARLVGVI, 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             86 ARLVGVL 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AB1598
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             d
C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A:Title: Genomic sequence comparison of two unrelated isolates of the human quatric path
A:Reference number: A71800; MUID:99120557; PMID:9923682
A;Accession: G71916
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A.Cross-references: GB.AEC01489; GB.AEC01439; NID:g4155102; PIDN:AADC6145.1; PID:g415511
A.Experimental source: strain J99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Species: Helicobacter pylori
A;Variety: Strain J99
C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 22-Jun-1999
C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 22-Jun-1999
C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 22-Jun-1999
C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999
C;Date: 12-Feb-1999
C;Date: 13-Feb-1999
C;Date: 13-Feb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein T15B3.160 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-car cress)
C:Species: Arabidopsis thaliana (mouse-car cress)
C:Species: Or-Jun-2000 *sequence_revision 02-Jun-2000 *text_change 18-Aug-2000
C:Accession: T48956
R:Jordan, N.: Bangert, S.: Wiedelmann, R.; Voss, H.; Unseld, M.: Newcs, H.W.; Rudd, submitted to the Protein Sequence Database, April 2000
                                                                                                                                                                                 \ddot{\circ}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              50.00
                                                                                                                                                                                            Gabs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .;
O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Map position: 3
A;Introns: 102/3; 115/1; 143/1
C;Superfamily: Arabidopsis thaliana hypothetica: protein 115B3.160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A:Residues: 1.159 <./UN>
A:Residues: 1.159 <./UN>
A:Cross-references: EMBL:AL163975; GSPDB:GN00661; ATSP:T15B3.160
A:Experimental source: cultivar Columbia; BAC clone T15B3
                                                              Length 141;
                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 173;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          inorganic pyrophosphatase - Helicobacter pylori (strain 399)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 3.5%; Score 7; DB 2; Best Local Similarity 100.0%; Pred. No. 19; Matches 7; Conservative 0; Mismatches
                                                                    DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ouery Match 3.5%; Score 7: DB 2; Best Local Similarity 100.0%; Pred. No. 17; Matches 7; Conservative C; Mismatches
                                                              3.5%; Score 7; DB 2; 100.0%; Pred. No. 15;
                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Gene: ppa
C;Superfamily: inorganic pyrophosphatase
     Ouery Match
Best Local Similarity 100.0
The Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Reference number: 225009
A;Accession: T48956
A;Status: preliminary
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 ALSLFLG 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 94 ALSLFLG 100
                                                                                                                                                                                                                                                                                        149 VGFCGIG 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                42 VGFCGIG 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12 ARLVGVL 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-173 <ARN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Gene: ATSP:T15B3.160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 10
D64597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 9
                                                                                                                                                                                                                                                                                                                                                                                         g
```

Ġ

Gaps

6

Length 202; 0; Indels

DB 2;

```
type TV pilus assembly protein Pilv, probable NMBO887 (imported) - Neisserla maningi CiSpecies: Noisserla meningicidis
Ripetrolin. H: Saunders, N.J.: Hoidelberg, J.: Jeffrics, A.C.: Nolson, K.E.: Ilsen, Mickey, B.K.: Haft, D.H.: Salzberg, S.L.: Write, O.: Fleischmann, R.D.: Dougherty, B. Ti, B.: Olin, H: Vamathevan, J.: Gill, J.: Scarlato, V.: Masignani, V.: Pizza, M. Science 287, 1809-1815, 2000
A;Atthors: Grandi, G.: Sun, L.: Smith, H.O.: Fraser, C.M.: Moxon, E.R.: Rappuoit, R. A;Title: Complete genome sequence of Neisserla meningitidis serogroup B strain MC58. A;Reference number: A81000; MUID:2017575; PMID:10710307
A;Residues: 1-204 <TET>
A;Reperimental source: serogroup B, strain MC58
A)Status: preliminary
A:Molecule type: DNA
A:Residues: 1-202 < KUNA
A:Cross-references: GB:BAR003018; PID:g13701150; PiDN:BAB42445.1; GSPDB:GN00149
A:Experimental source: strain N315
A:Experimental source: strain N315
C:Genetics:
A:Gone: SA1187
C:Superfamily: Escherichia coli ygiH protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 3.5%; Score 7; DB 2
Best Local Similarity 100.0%; Pred. No. 22;
Matches 7; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                             Ouery Match 3.5%; Score 7; DB 2
Best Local Similarity 100.0%; Pred. No. 22;
Matches 7; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Search completed: September 26, 2003, 17:42:36 Job time: 47.6979 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               137 CKDSSGN 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              113 AVATSAG 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  85 CKDSSGN 91
                                                                                                                                                                                                                                                                                                                                                                                                                                30 AVATSAG 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Gene: NMB0887
                                                                                                                                                                                                                                                                                                                                                                                                                                       ŝ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Aubtils Ynes protein homolog lmol284 (imported) - Listeria monocytogenes (strain EGE C. Species: Listeria monocytogenes (strain EGE C. Species: Listeria monocytogenes (c) Species: Prangeul, L.; Buchrieser, C.; Amend, A.: Baquero, F.; Fangeul, C.; Buchrieser, C.; Durand, E.; Durand, E.; Durand, E.; Durand, E.; Madueno, E.; Mattouriam, A.: Mascienes, L.; Kuhn, M.; Kunst, F.; Kurapkat, C.; Madueno, E.; Maitouriam, A.: Mascienes, Refer. T.; Simoce, N.; Tiatrez, A.; Vazquez-Boland, J.A.; Voss. E.; Weiliand, A.; Title: Comparative genomics of Listeria species. Rollond, J.A.; Voss. E.; Weiliand, A.; Title: Comparative genomics of Listeria species. Rollond, J.A.; Voss. E.; Weiliand, A.; Malecule type: DNA A.; Molecule type: C) Section of Sponics (Granderics: Strain EGD-e C); Superimental source: strain EGD-e C; Superfamily: Escherichia coli ygiii protein
      .; Dominguez Bernal, G.; Duchaud, E.; Durand, A.; Baguero, F.; Berche, F.; Siberker, Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A.Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madienc, E.; Mattourham, A.; M. A.Authors: Kreft, J.; Kuhn, M.; F.; Kurapkat, G.; Madienc, E.; Mattourham, A.; M. A.; Keference numbor: ABIO7; MUD:2153/279; PMID:11679669
A.Status; preliminary
A. Molecule type: D.A.
A. Molecule type: D.A.
A. Molecule type: D.A.
A. Molecule type: D.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ÷
                                                                                                                                                                                                                                                                                                                                                        A;Residues: 1-198 <GLA>
A;Cross-references: GB:AL592022; PIDN:CAC96554.1; PLD:gl6413795; GSFUB:GN05178
A;Experimental source: strain Clip11262
G;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Saps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Saps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .;
()
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ::
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7. Match 3.5%: Score 7: DB 2: Length 198:
Local Similarity 100.0%; Pred. No. 21;
les 7: Conservative 0; Mismatches C: Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 198;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         O: Indeis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 3.5%; Score 7; DB 2; Best Local Similarity 100.6%; Pred. No. 21; Matches 7; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A,Gene: lin1323
C.Superfamily: Escherichia coli ygiH protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       109 AVATSAG 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        109 AVATSAG 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30 AVATSAG 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30 AVATSAG 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               엄
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ें
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        a
```

O,

Gaps

. 0

Length 204; 0; Indels

DB 2;

```
September 26, 2003, 17:28:28; Search time 24.068i Seconds (without alignments) 394.688 Million cell updates/sec
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Octd.
                                                                                                                 OM protein - protein search, using sw model
                                                                                                                                                                     Run on:
```

US-09-852-100A-2_COPY_68_269 202 1 PSGPSAPEAVTARLVGVLWF......TRUTRLSIINETERKTOLVP 202 Title: Perfect score: Sequence:

OLIGO Gapop 60.0 , Gapext 60.0 Scoring table:

127863 seqs, 47026705 residues Searched:

127863 Total number of hits satisfying chosen parameters: 0 Word size :

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

SwissProt_41:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Bescription	, or	myscba											09a070 streptococc		_	P56750 homo sapien			Q20365 caenerhabd:	P55735 homo sapien	rhodo			Q10286 schizosacch	P53670 rattus norv			P20120 pisum sativ	09bz97 homo sapien		8x7h5	escherich	C9kcf9 bacillus ha
SUMMARIES	JD		YD86_MYCTU	YPAE_STRGC	IPYR_HELPJ		YC84_LISMO	YD23_LISIN	YA35_STAEP	YD53_STAAM	YC11_STRMU	YC30_STRA3	Y851_STRPN	Y908_STRPY	YKAC_LACI.A	YPJC_BACSU	CLDH_HUMAN	FABG_CHLTR	SDB2_MOUSE	RB33_CAEEL	SC13_HUMAN	CYB_RHOVI	CG51_HUMAN	CEAR_ECOLI	ITR1_SCHPO	LIK2_RAT	CNG2_BOVIN	AG43_ECOLI	PSAG_PEA	TY13_HUMAN	PUFX_RHOSH	PTKB_ECOL6	- 1	YG12_BACHD
	DB		Н	<b>-</b> +	_	-	-		rН		-	-	_	-	-	-	~	_	~	-	_	-	-	-	-	г	-	М	~	-	e-4	۲1	-	-
	Length		102	168	173	173	198	198	202	202	212	212	213	213	213	215	224	247	292	307	322	419	469	510	575	638	663	1039	39	58	82	94	75	111
gip.	Query Match	4.0		3.5																3.5												3.0		3.0
	Score	80	7	7	7	<i>(</i> -	7	7	Ĺ	Ĺ	7	7	7	(~-	7	7	7	7	7	7	7	7	7	7	7	7	7	7	9	9	9	9	9	9
	Result No.	1	2	e	4	Ŋ	9	7	80	6	10	11	12	13	14	1.5	9.	17	87.	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33

98xjp2 clostridjum P06017 trypanosoma P06066 macropus ru 043653 homo sapien 095xal mycobacteri 006327 mycobacteri P81649 sus scrofa 08tw26 methanopyru 08xaa sscherichia P45465 escherichia	SNTS	358 AA.	ence update) tation update) KKIALNE (EC 2.7.:) (Cyclin-dependent	a; Vertebrata; Eutcleostomi; ini; Hominidae; Homo.	Su LK., Gorka C., Nelson C., Lein kinases."; HR FAMILY OF PROTEIN KINASES.	right. It is produced through a collaboration of Bloinformatics and the EMBL outstation institute. There are no restrictions on its lions as long as its content is in no way is not removed. Usage by and for commercial spreement (see http://www.isb-sib.ch/announce/isb-sib.ch).		otein kinase activity; TAS. phosphoryiation; TAS. cycle; TAS.	RAMAT; SM00220; S_TKc; 1.  PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.  PROSITE; PS001019; PROTEIN_KINASE_ATP; 1.  PROSITE; PS00011: PROTEIN_KINASE_DOM: 1.  Transferase; Serine_threonine_protein kinase; ATP-binding.  Transferase; Serine_threonine_protein kinase; ATP-binding.  DOMAIN 5 28 PROTEIN KINASE.  NP_BIND  NP_BIN
YH14_CLOPE VSA8_TRYBB NNP_MACRU PSCA_HUMAN RS13_MYCLE RS13_MYCTU RS13_MYCTU RS13_MYCTU RS13_MYCTU RS13_MYCTU RS13_MYCTU YSA1_ECO57 YRAN_ECO57 YRAN_ECO57 YRAN_ECO57	ALIGNMENT	PRT;	created) Last sequence u Last annotation	ı; Craniata; V ;; Catarrhini;	99063; I.CL., Su ited protei HE SER/THR	yright. Institute Institute It is not re agreement	OINED.	pendent paint acid no acid no cell inase.	S_TKC; 1. ? PROTEIN_KINASE_ATF; 1. ?; PROTEIN_KINASE_ST; 1. 1: PROTEIN_KINASE_DOM; 1. ?; PROTEIN_KINASE_DOM; 1. ? 288 PROTEIN KIN 19 ATP (BY SIM 34 ATP (BY SIM 127 BY SIMILARI AA; 41834 MW; 88344321F AA; 41834 MW;
			Create Last s Last a in kin	rdata nates	1=163 Wu -rela -rela 52).	s cop itute tics stitu ment ment ense	11: 30	n-der in an atior ot_k; r_th; 1.	1. IN_K: IN_K: IN_K: Seonir
1122 1122 1222 1222 1231 1231 1231 1231		STANDARD;	Ψ.	nan). Da; Chordata ia; Primates	P. PubMecers G.H. LH. Dan cdc22917(1958ELONGS	entry is ss instinformal fit ins s statem s a lice to lice	A47002 A47002 383 CDK:1	F:cyclin P:prote P:regul: 719; Pro 290; Ser Kinase;	S_TKC; ; PROTE; ; PROTE ; PROTE ine/thr 288 19 34 127 127
		SI	(Rel (Rel (Rel onine	s (Hur Metazc utheri 9606;	OM N.447325, Ender Isai If humi	PROT (e Switten Bloom of this during quires email	8; CA. 9; CA. ; S23. 1; 1H(::1781.	693; 693; 674; PR000 PR002; 69; pD	220; S. 00100; 00108; 550011; 5 5 11 34 127 358 AA
2 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4		ET 1 _HOMAN KKIA_HUMAN	01-APR-1993 (Rel. 25, 01-APR-1993 (Rel. 25, 01-APR-1993 (Rel. 25, 15-OCT-2001 (Rel. 40, Serino/Chreonine-prot kinase-like 1).	CDKL1. Homo sapien. Bukaryota; P. Mammalia; E. NCB1_TaxID=9	SEQUENCE FROM N.A. MEDLINE=92347325; PubMed=1639663; MEDLINE=92347325; PubMed=1639663; MEDLINE=1. Nu CL. Harlow E., Isai L. H.: "A family of human cdc2-related p EMBC J. 11.2909-2517(1592)! SIMILARITY: BELONGS TO THE SE -! CDC2/CORX SUBFAMILY.	This SWISS-PROT entry is copyright. It is between the Swiss Institute of Bioinformatics Lostitute. The European Bioinformatics Institutions as long modified and this statement is not removed entities requires a license agreement (Secons end an email to license@isb.ch).	EMBL: X6635 EMBL: X6635 PIR: S23383 HSSP: P2494 Genew: HGNC Genew: HGNC	MIM; 003491 GO; GO: 6004 GO; GO: 6000 InterPro; I InterPro; I Pfam; PF000 Probom; PD0	SMART: SMOO PROSITE: PS PROSITE; PS Transferase DOMAIN NP BIND BINDING ACT SITE SEQUENCE
		RESU: ID	200 200 200 200 200 200 200 200 200 200	8 0 0 0 8 8	- 20 M M M H = 10 C	888888888	68888888	2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	ROUNDER HER CO.

a

ó

Gaps

ij

indels

.. ()

Misma:ches

်

```
7; Conservative
                                                                                                                                                                                                                                                  NCBI_TaxID=29390;
                                                                                                                                                                                                                                       Streptococcus
                                                                                                                                                                                                                                                                                                                                   gordonii CH1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1PYR_HELPJ
09ZLL5;
                                                                                                                           YPAE_STRGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IPYR_HELPJ
                                                                                                               YPAE_STRUC
  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3
                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation the European Bloinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is 15 no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/annchncc/or send an email to license@isb-sib.ch).
                                          ..
(2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-CDC 1551 / Oshkosh;
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Peterson J., DeBoy R., Dodson R., Gwin M.L., Haft D., Hickey E.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolacey K.D., Salzberg S.L.,
Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
                                                                                                                                                                                                                                                                                                                                                                                                                   s;
                                            Gaps
                                                                                                                                                                                                                                                                                                                                                        MEDLINE-9829597; Pubmed-9634230;
Cole S.T., Brosch R., Parkhili J., Garnier I., Churcher C., Harris J. Cole S.T., Brosch R., Parkhili J., Garnier I., Churcher C., Harris J. Gordon S.V., Eiglmeet K., Gas S., Barry C.E. III, Tekklar F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S., Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell H.G.; "Deciphering the biology of Mycobacterium tuberculosis from the Complete genome sequence.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Whole genome comparison of Mycobacterium tuberculosis clinical and
                                                                                                                                                                                                                                                                              Bacteria, Actinobacteria, Actinobacteridae: Actinomynetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL. HYPOTHETICAL PROTEIN RV1386.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 102;
              Length 358;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    laboratory strains.; Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
                                          0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8165F09DBDB9D752 CRC64;
                                                                                                                                                                                                                                                                                          Corynebacterineae, Mycobacteriaceae, Mycobacterium
NCBI_faxID=1773;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TIGR. WT1430;
--
TUBECTGLISEL, RV1386;
--
INTERPTO: IRRO00084; PE_region.
Pfam. PF00934; PE, 1.
Hypothetical protein; Signal; Complete proteome.
                                                                                                                                                                                         30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
28-FEB-2003 (Rel. 41, Last annoration update)
PAPPED-2003 (Rel. 41, Last annoration update)
RV1386 OR MI1430 OR MTCY2184,03.
              DF 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1;
. 6.5;
                                         0; Mismatches
              4.0%; Score 8; [
100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 7; 1
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              102
: 9862 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AE307014; AAK45695.1; -.
PIR; H70898; H70898.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3.5%; S
100.0%;
                                                                                                                                                                                                                                                                Mycobacterium tuberculosis.
Ouery Match
Best Local Similarity 100...
8. Conservative
                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; 280108; CAB02191.
                                                                     138 YPALGLIK 145
                                                                                              259 YPALGLLK 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE 102 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN-H37RV:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                   MYCTU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bishai W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted
                                                                                                                                                                 YD86_MYC
P71656;
                                                                                                                                                                    ő
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMB: outstation: the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce, or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ö
                                                                                                                                                                                                                                                                                                                                                                Vriesema A.J., Dankert J., Zaat S.A.; "Isolation and characterization of promoter regions from Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30.MAY-2006 (Rel. 39, Created)
30.MAY-2006 (Rel. 39, Last sequence update)
28-PEB-2003 (Rel. 41, Last annotation update)
28-PEB-2003 (Rel. 41, Last annotation update)
Inorquanic pyrophosphatase (EC 3.6.1.1) (Pyrophosphate phospho-
PPA OR JHP0564.
Helicobacter pylori 399 (Campylobacter pylori J99).
Bacteria: Proteobacteria: Epsilonproteobacteria: Campylobacterales;
NCBL_TAXID=85963;
                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
-: SUBCELLULAR LOCATION: Integral membrane protein (Potential).
-: SIMILARITY: BELONGS TO THE UPF0078 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ö
                                                                                                                                                           Length 168;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17921 MW; A07262BD799A478A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 7; DB 1;
Pred. No. 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               173 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Pred. no.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hypothetical protein; Transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AJ236899; CAB40549.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DUF205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  131
164
168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HAMAP; MF_01043; -; 1.
InterPro; IPR003811; DU
Pfam; PF02660; DUF205;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Olery Match
Bost Local Similarity
The 7: Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     106 AVATSAG 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        168 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30 AVATSAG 36
8 EAVTARL 14
                     SEQUENCE FROM N.A.
```

```
28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12 ARLVGVL 18
                                                                                                                                                                                                                                                                               ; D64597
                                                                                                                                                                                                                                                                                              P17288; IFAJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YC84_LISMO
Q8Y7J3; Q8KYA9:
                                                                                                                                                                                                                                                                                                            TIGK; HP0620;
  Venter J.C.;
                                                                                                                                                                                                                                                                                PIR; D64597
HSSP; P1728
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-EGD;
                                                                                                                                                                                                                                                                                                                                                                                                      ACT_SITE
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LM01284.
  2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the FWBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN-26695 / ATCC 700392;
MEDLINE-97394467; PubMed-922185;
Tomb J. F., White O., Kerlavage A.R., Clayton R.A., Sutton G.G.,
Tomb J. F., White O., Ketchum K.A., Klenk H.-P., Gill S., Doughcrty B.A.,
Fleischmann R.D., Ketchum K.A., Klenk H.-P., Gill S., Doughcrty B.A.,
Nelson K., Quackenbush J., Zhou L., Kirkness E.F., Peterson S.,
Loftus B., Richardson D., Dodson R., Khalak H.G., Glodek A.,
McKenney K., FitzGerald L.M., Lee N., Adams M.D., Hickey E.K.,
McKenney K., FitzGerald L.M., Lee N., Adams M.D., Hickey E.K.,
Berg D.E., Gocayne J.D., Utterback T.R., Peterson J.D., Kelley J.M.,
Cotton M.D., Weidman J.M., Filji C., Bowman C., Watthey L., Wallin E.,
Hayes W.S., Borodovsky M., Karp P.D., Smith H.O., Fraser C.M.,
           MEDLINE=99120557; PubMed=9923682; Alm R.A., Ling L.-S.L., Brown E.D., Doig P.C., Alm R.A., Ling L.-S.L., Moir D.T., King B.L., Brown E.D., Doig P.C., Smith D.R., Noonan B., Guild B.C., deJonge B.L., Carmel G., Tummino P.C., Caruso A., Uria-Nickelsen M., Mills D.M., Tves C., Gibson R., Merberg D., Mills S.D., Jiang Q., Taylor D.E., Vovis G.E., Trust T.J.,
                                                                                                   80.88
                                                                                           *Genomic sequence comparison of two unrelated isolates of the human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Helicobacter pylori (Campylobacter pylori).Bacteria: Proteobacteria: Epsilonproteobacteria: Campylobacterales:Helicobacteraceae: Helicobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ċ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-Rol 41, Last annotation update)
Inorqanic pyrophosphatase (EC 3.6.1.1) (Pyrophosphate phospho-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6; Indels
                                                                                                                                                                                   -:- SUBUNIT: Homohexamer (By similarity).
-:- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-:- SIMILARITY: Belongs to the PPase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    87B9B215E6FEBFC8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            :: BO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              173 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                              Interprior 188001596; Pyrophosphatase. Pfam: PF06719; Pyrophosphatase: 1. Probom: PF062719; Pyrophosphatase: 1. ProSITE; PS00387; PPASE; 1. PROSITE; PAGESE: Complete proteome. ACI. SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                EMBL, AE001489; AAD06146.]; --
PIR; G71916; G71916.
HSSP; P17288; 1FAJ.
HAMAP; MF_30209; --; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACT_SITE 28 28 B
SEQUENCE 173 AA; 19258 MW:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Owery Match
Best Local Similarity 100.0%:
Marches 7: Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12 AREVGVL 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         86 ARLVGVL 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (PPase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID-210;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PPA OR HPC620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IPYR_HELPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hydrolase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P56153;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IPYR_HELPY
ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          q
```

```
This SWISS-PROI entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                             -: - CATALYTIC ACTIVITY: Diphosphate + H(2)0 + 2 phosphate.
-:- COFACTOR: REQUIRES THE PRESENCE OF DIVALENT METAL CATION.
MAGNESIUM CONFERS THE HIGHEST ACTIVITY. BINDS 4 DIVALENI CATIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE—21537279: PubMed=11679669;
MEDLINE—21537279: PubMed=11679669;
Glaser P., Frangeul L., Buchrieser C., Rusniok C., Amend A.,
Glaser P., Terangeul L., Buchrieser C., Rusniok C., Amend A.,
Charbit A., Chetouani F., Couve E., de Daruvar A., Dehoux P.,
Domann E., Dominguez Bernal G., Duchaud E., Durant L., Dussurget O.,
Entian K.-D., Fsihh H., Garcia-del Portillo P.,
Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,
Jones L.-M., Kaerst U., Kreft J., Kuhn M., Kunst F., Kurapkat G.,
"The complete genome sequence of the gastric pathogen Helicobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lampidis R., Kostrewa D., Hof H.:
"Molecular characterization of the genes encoding DNA gyrase and
topoisomerase IV of Listian monocytogenes.";
J. Antimicrob. Chemother. 49:917-924(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Listeria, monocytogenes.
Racteria, Firmicutes, Bacillales, Listeriaceae, Listeria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 173;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                     PER SUBUNIT (BY SIMILARITY).
--- SUBUNIT: HOMOHORAMER (By Similarity).
--- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
--- SIMILARITY: Belongs to the PPase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BY SIMILARITY.
23A51C685A6EC7F2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3.5%; Score 7; DB 1; 100.0%; Pred. No. 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28 FEB-2003 (Rel. 41, Created)
28 FEB-2003 (Rel. 41, Last sequence update)
28 FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred No. 13;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        198 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hydrolase; Magmesium; Complete proteome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HAMAP; MF_00209; -; 1.
interPro; IPR001596; Pyrophosphatase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam, PF00719; Pyrophosphatase; 1. ProDom: PD602014; Inorg_pphsph; 1. PROSITE; PS00387; PPASE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=22035523; PubMed=12039883;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AE000576; AAD07684.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 173 AA: 19272 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hypothetical protein Lmo1284.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cuery Match
Best Local Similarity 100.vv
                                                                Nature 388:539-547(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its mose by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and tor commercial entities requires a license@isbent(See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                        \ddot{\circ}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TRAIN-CLIP 11262 / Serovar 6a:

C STRAIN-CLIP 11262 / Serovar 6a:

C MEDLINE-2153729; pubMed-11679669;

A Glaser P., Frangeul L., Buchrieser C., Rusnick C., Affend A.,

A Glaser P., Frangeul L., Buchrieser C., Edarwar A., Dehovix P.,

A Gharbit A., Chectouani F., Couve E., de Darwar A., Dehovix P.,

A Domann E., Dominguez Bernal G., Duchaud E., Durant L., Cussurget C.,

A Domenn E., Marcia Gomez-Lopez N., Hain T., Haul C., Cussurget C.,

A Jones L.-M., Kaerst U., Kreit J., Khin M., Kunst F., Kripapkat S.,

A Jones L.-M., Mata Vicente J., Ng F., Nedjari H.,

RA Madueno E., Maitournam A., Mata Vicente J., Ng F., Nedjari H.,

RA Madueno E., Maitournam A., Mata Vicente J., Ng F., Nedjari H.,

RA Madueno E., Maitournam A., Mata Vicente J., Ng F., Nedjari H.,

RA Memmel B., Rose M., Schlueter T., Simoes N., Tierrez A., Purcell E.,

RA Vazquez-Boland J.-A., Voss H., Wehland C., Cossart P.,

Comparative genomics of Lasteria species.";
                                                                                                                                                                                                                                                                                                                                                                                                                                        Caps
         .;
O
Madueno E., Maitournam A., Mata Vicente J., Ny E., Nedjari H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Firmicutes; Bacillales; Listeriaccae; Listeria
NCBL_TaxID=1642;
                                                                                                                                                                                                                                                                                                                                                                                                                DB 1: Length 198;
. 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                        C; Indels
                                                                                                                                                                                                                                                                                                 Complete proteome.
                                                                                                                                                                                                                                                                                                                                                      IFY -> FST (IN REF. 1).
N -> I (IN REF. 1).
D -> V (IN REF. 1).
7807B5406DF65GDI CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28-FEB-2003 (Rei. 41, Created)
28-FEB-2003 (Rei. 41, Last sequence update)
48-FEB-2003 (Rei. 41, Last annotation update)
Hypothetical protein Linl323.
                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Pred. w...
                                                                                                                                                                                                                                                                                                                                                                                                               3.5%; Score 7; D
(00.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                     POTENTIAL.
POTENTIAL.
POTENTIAL.
                                                                                                                                                                                                                                                                                                         POTENTIAL.
                                                                                                                                                                                                                                                                 pfam; PF02660; DUF205; 1.
TIGREAMS; TIGRO0023; Transmembrane;
Hypothetical protein; Transmembrane;
TRANSMEM 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                EMBL; AF084044; AAM48493.2; ... EMBL; AL591978; CAC99362.1; ... PIR; AD1235; AD1235.
                                                                                                                                                                                                                                                                                                                                                                             62 D
21599 MW;
                                                                                                                                                                                                                                    Listifist; LMOC1284; -.
HAMAP; MF_01043; -; 1.
Interpro; IPR003811; DUF205.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Science 294:849-852(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     109 AVATSAG 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                30 AVATSAG 36
                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Listeria innocua.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YD23_LISIN
Q92C58;
                                                                                                                                                                                                                                                                                                                                                        CONFLICT
CONFLICT
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                             InterPro:
                                                                                                                                                                                                                                                                                                                        TRANSMEM
                                                                                                                                                                                                                                                                                                                                  TRANSMEM
                                                                                                                                                                                                                                                                                                                                              TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
```

```
This SWISS-PROI entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its meet by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation here are no restrictions on its use by non-profit institutions as long as its content is in no war modified and this statement is not removed. Usage by and for commercia entities requires a license agreement (Sec http://www.isb-sib.ch/announce, or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Saps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        . 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN-ATCC 12228;
Zhang Y., Ren S., Di H., Fu G., Lu L., Lu G., Jia J., Tu Y., Oin
Chen Z., Wen Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
-!- SIMILARITY: BELONGS TO THE UPF0078 FAMILY.
-:- SUBCELLULAR LOCATION: Integral membranc protein (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 198:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C: Indeis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL: AL596.68; CAC96554.1;
PIR; AB1598; AB1598.
FIRSTILIST: LING1323:
FAMAP. M. FOL043:
FORM: PF0266; DUP205.
FIGHERPR: TIGR0023: TIGR00023; TIGR00023; TIGR00023; TIGR00023: T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HAMAP; MF_01043; -: 1.
Pfam, PP02660; DUF205; 1.
TIGREDAM; TIGREDOZ3: TIGREDOZ3: 1.
Hypothetical protein; Transmembrane; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            114 136 POTENTIAL.
156 178 POTENTIAL.
198 AA: 21632 MW; B161D1055R203406 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Staphylococcus epidermidis.
Bacteria; Firmicutes: Bacillales; Staphylococcus
NCHI_TaxID=1282;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Guery Match 3.5%; Score 7; DB 1; Best Local Similarity 100.0%; Pred. No. 15; Matches 7; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Hypothetical protein SE1035.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    202 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POTENTIAL.
POTENTIAL.
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AE016747; AA004632.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27
107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26
74
106
140
151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              109 AVATSAG 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30 AVAISAG 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YA35_STAEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TRANSMEM
TRANSMEM
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TRANSMEM
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TRANSMEM
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P59253;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YA35_STAEP
```

Gaps

::

0; Indels

3.5%; Score 7; DB 1; Length 202; 00.0%; Pred. No. 15;

100.0%; Pred. ....

30 AVATSAG 36

A9DA126B5731749C CKC64;

POTENTIAL. POTENTIAL.

POTENTIAL

```
9.5
Sest Local Similarity 100.
Matches 7; Conservative
                                               TRANSMEM
SEQUENCE
TRANSMEM
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AC ID
                                                                                                                                                                                                                                                                                                                                                                                                         SO THE TRANSPORT OF THE PARTY O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ô
  FT
FT
SO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMES cutstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb.ch/announce.or send an email to license@lsb.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ं
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEGNENCE FROM N.A.
SEGNENCE FROM N.A.
SETRAIN-MUSO / A TCC 700699, and N315;
MEDLINE-21311952; PubMed=11418146;
Kuroda M., Ohta T., Uchiyama T., Baba T., Yuzawa H., Kobayashi I.,
Kuroda M., Ohta T., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
Kanebhisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.,
Whole genome sequencing of meticillin-resistant Staphylococcus
                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-22040717; PubMed-12044378;
Baba I., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oquchi A.,
Baba I., Takeuchi F., Kuroda M., Yuzawa H., Coli L.,
Yamanoto K., Hiramatsu K.;
"Genome and virulence determinants of high virulence community-
acquired MRSA.";
                                                                                                                     ö
                                                                     DB 1; Length 202;
                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HAMAP: ME_01043; -: 1.
InterPro: 1PR003811; D0F205.
Figh: PF0560; D0F205; 1.
FIGROMS: TIGRO0023; TIGRO0023; 1.
FYPOThetical protein; Transmembrane; Complete proteome.
TRANSMEM 4 26
POTEWIIAL.
FRANSMEM 52 74
POTEWIIAL.
FRANSMEM 84 106
POTEWIIAL.
                      202 AA; 22105 MW; 6516AFA775DD72E0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Staphylococcus aureus (strain Mus5) / ATCC 700695), Staphylococcus aureus (strain M15), and Staphylococcus aureus (strain MW2).

Bacteria: Firmicutes: Bacillales; Staphylococcus. NCBL_Tax1D=158878, 156879, 196620:
                                                                                                                                                                                                                                                                                                                                                                           28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
49-FEB-2003 (Rel. 41, Last annotation update)
SAVI353 OR SAI187 OR MW1240.
                                                                                                                                                                                                                                                                                                                                   202 AA
                                                                     3.5%; Score 7; DB 3
100.0%; Pred. No. 15;
Live 0; Mismatches
POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AP003362; BAB57515.1; -. EMBL; AP003133; BAB42445.1; -. EMBL; AP004826; BAB95105.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lancet 357:1225-1240(2001).
                                                 Query Match
Best Local Similarity 100.
The 7; Conservative
                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                            113 AVATSAG 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PIR; A89911; A89911.
HAMAP; MF_01043; -;
                                                                                                                                                                 30 AVATSAG 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. STRAIN=MW2;
                                                                                                                                                                                                                                                                                                                                   YD53_STAAM
TRANSMEM
                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     aureus.
                                                                                                                                                                                                                                                                                                                                   à
                                                                                                                                                                                                              Ω
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL cutstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announcc/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ..
0
                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN=0A159, ArcC 700610 / Serotype C;
MEDLINE=22295063: PubMed=12397186:
Ajdic D., McShan W.M., McLaughlin R.E., Savic G., Chang J.,
Carson M.B., Primeaux C., Tian R., Kenton S., Jia H., Lin S., Qian Y.,
Li S., Zhu H., Najar F., Lai H., White J., Roe B.A., Ferretti J.J.;
'Genome sequence of Streptococcus mutans UA159, a cariogenic dental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps

    Proc. Natl. Acad. Sci. U.S.A. 99:14434-14439(2002).
    SUBCELLULAR LOCATION: Integral membrane protein (Potential).
    SIMILARITY: BELONGS TO THE UPPO078 FAMILY.

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 7; DB 1; Length 212;
Pred. No. 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                                                                   Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hypothetical protein; Transmembrane; Complete protecme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL.
D44DA5F4270C5F5B CRC64;
                                                                                                                                                  28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
99/0.1211.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      212 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL. POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HAMAP: MF_01043; -: 1
Pfam; PF02660; DUF205; 1.
TIGRFAMS; TIGR00023; TIGR00023: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AE014958; AAN58897.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23417 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3.5%; 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100...
7; Conservative
                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                               Streptococcus mutans
113 AVATSAG 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             140 1
166 1
212 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           105 AVATSAG 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30 AVATSAG 36
                                                                                                                                                                                                                                                                                                                                                                    NCEL_TaxID=1309;
                                                                                                                                                                                                                                                                                                                                             Streptococcus
                                                                                                                     YC11_STRMU
P59255;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YC30_STRA3
P59254;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YC30_STRA3
                                                                                              YC11_STRMU
```

213 AA

STANDARD;

9

```
Y851_STRPN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce) or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACTION OF A SET OF A 
                                                                                                                                                                                                                                                                                                                                    STRAIN*NEM316 / Serotype III;
MEDLINE-2224508; Bubmed-123521;
Glaser P., Rusniok C., Buchrideser C., Chevaller F., Frangeul I..,
Msadek T., Zomine M., Couve E., Lalioul L., Poyart C., Triew-Cust P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Complete genome sequence and comparative genomic analysis of an emerging human pathogen, serotype V Streptococcus agalactiae."; Proc. Natl. Acad. Sci. U.S.A. 99:12391-12396(2002).
-! SUBCELLUGAR LOCATION: Integral membrane protein (Potential).
-! SIMILARITY: BELONGS TO THE UPPO078 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Genome sequence of Streptococcus agalactiae, a pathogen causing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 212;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                     Streptococcus agalactiae (serotype III), and
Streptococcus agalactiae (serotype V).
Bacteria; Firmicutes; Lactobacillales: Streptococaccae:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hypotherical protein; Transmembrane; Complete protecme. TRANSMEM 4 23 POTENTIAL. TRANSMEM 69 91 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2BFE4A06F04E1687 CRC64;
                       28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Hypothetical protein qbs1230/SAG1155.
GRSL1230 OR SAG1155.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 7; 1
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL. POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                vasive neonatal disease.";
1. Microbiol. 45:1499-1513(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HAMAP, WF_01643; -, 1
Pfam; PF02660; DUF205; 1,
TIGRFAWS; TIGR00023; TIGR00023; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ن
ن
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AL766849; CAD46889.1; -. EMBL; AE014244; AAN03037.1; -.
28-FEB-2003 (Rel. 41, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3.5%; £
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23403 MW;
                                                                                                                                                                                                                         Streptococcus.
NCBI_TaxID=216495, 216466;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SagaList; gbs1230; ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               69
113 1
142 1
168 1
212 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
es 7; Conserv
                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      invasive nechatal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                               Kunst
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
```

105 AVATSAG 111

RESULT 12 Y851_STRPN

30 AVATSAG 36

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-21357209; PubMed-11463916;
MEDLINE-21357209; PubMed-11463916;
Tettelin H., Nelson K.E., Paulsen I.T., Elsen J.A., Read T.D., Peterson S., Heidelberg J., DeBoy R.T., Haft D.H., Dodson R.J., Durkin A.S., Gwinn M., Kolonay J.F., Nelson W.C., Peterson J.D., Umayam L.A., White O., Salzberg S.L., Lewis K.R., Radune D., Khouri H., Wolf A.M., Utterback T.R., Hansen C.L., McDonald L.A., Feldblyum T.V., Angiuoli S., Dickinson T., Hickey E.K., Holt I.E., Loftus B.J., Yang F. Smith H.O., Venter J.C., Doughorty B.A., Morrison D.A., Hollingshead S.K., Fraser C.M.; **Complete genome sequence of a virulent isolate of Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-ATCC BAA-255 / R6;

STRAIN-ATCC BAA-255 / R6;

MEDLINE-2192045; Pubked-11544234;

MEDLINE-2192045; Pubked-11544234;

DeHoff B.S., Estrem S.T., Fritz L., Fu D.-J., Fuller W., Geringer C., Gilmour R., Glass J.S., Khoja H., Kraft A.R., Lagace R.E.,

LeBlanc D.J., Lee L.N., Lefkowitz E.J., Lu J., Matsushima P.,

MCAhren S.M., McHenney M., McLeaster K., Mundy C.W., Nicas T.I.,

Noris F.H., O'Gara M., Peery R.B., Robertson G.T., Rockey P.,

Sun P.-M., Winkler M.E., Yang Y., Young-Bellido M., Zhao G.,

Glass J.I.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Cloning and characterization of the parc and parE genes of Streptococcus pneumoniae encoding DNA topoisomerase IV: role in fluoroquinolone resistance.";
                                                                                                                                            Streptococcus pneumoniae (strain AICC BAA-255 / K6).
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HAWAP; MF_01043; -: 1.
InterPro; IPR003811: DUF205.
Pfam; PF02660; DUF205; 1.
IGRFAM; TGR00023; 1.
Hypothetical protein; Transmembrane; Complete proteome.
                                 15-JUL-1999 (Rel. 38, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-PEB-2003 (Rel. 41, Last annotation update)
Hypotherical protein SP0851/Spr0755.
                                                                                                                                                                                                                                                                                                                                                                   Bacteriol, 178:4060-4069(1996).
                                                                                                                                                                                                                                                                            MEDLINE-96312346; Pubmed-8763932;
Pan X., Fisher M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL: 267739; CAA91549.1; -. EMBL: AE007390; AAK74980.1; -. EMBL: AE008451; AAK99559.1; -.
                                                                                                                                Streptococcus pneumoniae, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              pneumoniae.";
Science 293:498-506(2001).
                                                                                                                                                                                                  NCB1_Tax1D=1313, 17110::
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PIR; C95098; C95098.
PIR; C97966; C97966.
                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                        SECUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TIGR; SP0851;
                                                                                                                                                                                  Streptococcus
                                                                                                                                                                                                                                                            STRAIN-7785
```

us-09-852-100a-2_copy_68_269.rsp

```
TRANSMEM
TRANSMEM
                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                        TRANSMEM
                                                                                                                                                                                                                                                                                    TRANSMEM
                                                                                                                                                                                                                                                                                                TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 14
YKAC_LACLA
                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         :
:
                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN=SP370 / ATCC 700294 / Serotype M1;
STRAIN=SP370 / ATCC 700294 / Serotype M1;
MEDLINE=21192684; PubMed=11296296;
Ferretti J.J., McShan W.M., Ajdic D.J., Savic D.J., Savic G., Lyon K., Primeaux C., Sezate S., Suvorov A.N., Kenton S., Lai H.S., Lin S.P., Qian Y., Jia H.G., Najar F.2., Ren Q., Zhu H., Song L., White J., Yuan X., Clifton S.W., Roe B.A., McLaughlin R.;
"Complete genome sequence of an M1 sirain of Streptococcus pyogenes.";
Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The genome of invasive Streptococcus pyogenes; a comparative analysis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-MGASB232 / Serotype M18;
MEDLINE=21927593; PubMed=11917108;
Smoot J.C., Barbian K.D., Van Gompel J.J., Smoot L.M., Chaussee M.S., Sylva G.L., Sturdevart D.E., Ricklefs S.M., Porcella S.F., Salva G.L.D., Beres S.B., Campbell D.S., Smith T.M., Zhang Q., Kapur V., Daly J.A., Veasy L.G., Musser J.M.;
"Genome sequence and comparative microarray analysis of serotype M18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-MGAS315 / Serotype M3:
MEDLINE=22133808; PubMed=12122256;
Beres S.B., Sylva G.L., Barbian K.D., Let B., Hoff J.S.,
Bammarella N.D., Liu M.-Y., Smoot J.C., Forcella S.F., Parkins L.L.,
Campbell D.S., Smith T.M., McCormick J.K., Leung D.Y.M.,
Schlievert P.M., Musser J.M.;
Genome sequence of a serotype M3 strain of group A Streptococcus:
phage-encoded toxins, the high-virulence phenotype, and clone
                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             group A Streptococcus strains associated with acute rheumatic fever
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-SSI-1 / Serotype M3;
Nakagawa I., Kurokawa K., Nakata M., Tomiyasu Y., Yamashita A.,
Yamazaki K., Okahashi N., Kawabata S., Yasunaga T., Hattori M.,
Hayashi H., Hamada S.,
                                                                                                                        ;
                                                                                                                                                                                                                                 1908_STRPY STANDARD, PRT; 213 AA. 094070; 0887U8; Created) 28-FEB-2003 (Rel. 41, Created) 28-FEB-2003 (Rel. 41, Last sequence update) 15-SEP-2003 (Rel. 41, Last snotation update; Hypothetical protein SPy0908/SpyM3_0623/SPs1230/spyM:8_0966. SPY0908 OR SPYM3_0623 OR SPYM18_0966.
                                                                                                  DB 1: Length 213;
                                                                                                                                                                                                                                                                                                                      Streptococcus pyogenes,
Streptococcus pyogenes (serotype M3), and
Streptococcus pyogenes (serotype M18).
Bacteria: Firmicutes, Lactobaciliales, Streptococcaccae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         of S. pyogenes SSI-1, SF370 and MCAS8232.":
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
                                                              S -> F (IN REF. 1).
22CB089C17750818 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Proc. Natl. Acad. Sci. U.S.A. 99:10078-10083(2002)
                                                                                          3.5%; Scole ,,
100.0%; Pred. No. 16;
           POTENTIAL.
POTENTIAL.
POTENTIAL.
 POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                      Streptococcus.
NCBI_TaxID=1314, 198466, 186103;
22
90
132
163
164
168
22928 MW;
                                                                                     Ouery Match
Best Local Similarity Juv...
7, Conservative
                                                                                                                                                                        105 AVATSAG 111
  2
112
143
164
168
                                                                                                                                                30 AVATSAG 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           emergence. ";
                                                              CONFLICT
                                     TRANSMEM
TRANSMEM
 TRANSMEM
              TRANSMEM
                           TRANSMEM
                                                                                                                                                                                                           RESULT 13
Y908_STRPY
                                                                                                                                                                                                                                     ô
                                                                                                                                                                        Ωp
 FT
FT
FT
FT
FT
SC
SC
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ز:
                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL Outstation the European Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lactococcus lactis (subsp. lactis) (Streptococcus lactis).
Bacteria: Firmicutes; Lactobacillales; Streptococcaccae; Lactococcus
outbreaks.";
Proc. Natl. Acad. Sci. U.S.A. 99:4668-4673(2002).
-!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
-!- SIMILARITY: BELONGS TO THE UPP6078 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .
C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 213;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Transmembrane; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6A9881232A09766A CRC64:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Hypothetical protein ykaC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3.5%; Score 7; DH 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL.
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POTENTIAL
                                                                                                                                                                                                                                                                                                                                       EMBL; AE006539; AAK33824.1; -.
EMBL; AE014149; AAM79230.1; ALT_INIT.
EMBL; AE005144; BAC64325.1; -.
EMBL; AE010024; AAL97607.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-21235186; PubMed-11337471;
                                                                                                                                                                                                                                                                                                                                                                                                                                             HAMAP, ME_01043; -; 1
InterPro: IPR003811; DJF205.
Pfam: PF02560; DUF205; 1
IIGREAMS; TIGR00023; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                110 132 PO
139 161 PO
166 183 PO
213 AA; 23369 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AE006332; AAK05076.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Overy Match
Bost Local Similarity loves
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PIR; B86747; B86747.
HAMAP; MF_01043; -; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hypothetical protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   105 AVATSAG 1:1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30 AVATSAG 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Firmic
NCBI_TaxID=1360;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TRAC OR LL0978.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-IL1403;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YKAC_LACLA
```

```
RC STRAIN-168;

KR WEDLINE-98044033; PubMed-9384377;

KNDLINE-98044033; PubMed-9384377;

RA AZEVERCE, F. Ogasawara N., Moszer I., Albertini A.M., Alloni G.,

RA AZEVERO V., Bertero M.C., Bessieres P., Bolotin A., Borchert S.,

RA AZEVERO V., Bertero M.C., Brans A., Fraun M., Brignell S.C., Bron S.,

RA Borriss R., Boursier L., Brans A., Fraun M., Brignell S.C., Bron S.,

Bronilet S., Enuschi C.V., Caldwell B., Capuano V., Carter N.H.,

RA Choi S.K., Codani J.J., Connettor I.F., Cummings N.J., Daniel R.A.,

Britz C., Fujita M., Fujita Y., Fabret C., Ferrari E., Fouiger D.,

RA Entian K.D., Errington J., Fabret C., Ferrari E., Fouiger D.,

RA Guiseppi G., Guy B.J., Haga K., Halloh W.F., Itaya M., Jones I.,

RA Guiseppi G., Guy B.J., Haga K., Halech J., Harwood C.R., Henaut A.,

RA Hilbert H., Holappel S., Hosono S., Hullo M.F., Itaya M., Jones I.,

RA Kobayashi Y., Koetter P., Koningstein G., Krogh S., Kumano M.,

RA Kuita K., Lapidus A., Lardinols S., Hauber J., Lazarovic V.,

RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,

RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,

RA Presecan E., Pujic P., Purnelle B., Ropoport G., Rey M., Reynolds S.,

RA Scanlam E., Schleich S., Schroeter R., Scoflon F.,

RA Scrokin A., Tamakoshi A., Tamaka T., Takahashi H., Takamaru K.,

RA Sorokin A., Tamakoshi A., Tamaka T., Wallers P., Tognoni A.,

RA Tosato V., Uchiyama S., Vandenbol M., Vander P., Wasaantti A.,

Waita A., Wanbutt R., Wander E., Wodler E., Wallerseya A., Yanamoto H., Yanamato P., Wannengo K., Yata K.,

RA Tosato V., Uchiyama S., Vandenbol M., Vandenboger T.,

RA Hoters P., Wipat A., Yanamoto H., Yanamato C., Yasaanto L.,

RA Hoters P., Wipat A., Yanamoto H., Yanamato C., Yasaanto L.,

RA Hoters P., Waller E., Wander E., Wander E., Wasaanto L.,

RA Hoters P., Waller E., Wander E., Wander E., Waller E., Waller E., Waller E., Waller E., Waller E., Wall
                                                                                                                                                                                                                                                                                      Ġ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Sequence analysis of the Bacillus subtills chromosome region between
the serA and Kdg loci cloned in a yeast artificial chromosome.";
Microbiology 142:2005-2016(1996).
                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-168 / Marburg;
MEDLINE-96349105; PubMed-8760912;
Sorokin A.V., Azevedo V., Zumstein E., Galleron N., Ehrlich S.D.,
                                                                                                                                                                                                                                                                                      ..
                                                                                                                                                                                                                                           DB 1: Length 213:
                                                                                                                                                                                                                                                                                      0; indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
              Pfam, PF02660: DUF205; 1.
TIGREAMS: TIGR00023; TIGR00023; 1.
Hypothetical protein: Transmembrane; Complete proteome reansmem
                                                                                                                                                                                 POTENTIAL. 967258F000F31AE3 CRC54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    71-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                              3.5%; Score
100.0%; Pred. No. 10.
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      215 AA
                                                                                                                          POTENTIAL.
POTENTIAL.
                                                                                 POTENTIAL.
POTENTIAL.
                                                                                                                                                                POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                     23362 MW;
InterPro; 1PR003811; DUF205.
                                                                                                                                                                                                                              Ouery Match
Best Local Similarity 100.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hypothetical protein ypjC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                 106 AVATSAG 112
                                                                                                                     70
112 1
141 1
167 1
213 AA;
                                                                                                                                                                                                                                                                                                                          30 AVATSAG 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacillus subtilis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID-1423;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YPJC_BACSU
P42978;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Serror P.;
                                                                                                                     TRANSMEM
TRANSMEM
TRANSMEM
                                                                                                                                                                                 TRANSMEM
SEQUENCE
                                                                                                      IRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      a
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no war modified and this statement is not removed. Usage by and for commorcial entities requires a license agreement (See http://www.isb-sib.ch/announce, or send an emall to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ŝ
Yoshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.;
"The complete genome sequence of the Gram-positive bacterium Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                    -!- SUBCELLULAR LOCATION: Integral membrane proteim (Pouential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ő
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 215;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C; Indeis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; L38424; AAA92872.1; -.
EMBL; L47709; AAB38440.1; -.
EMBL; L299112; C5AB14167.1; -.
Sublitist; BG11209; ypjC,
InterPro; IRR003740; DNFf61.
Ffam; PPO2589; DNFf61.
Hypothetical protein: Transmembrane; Complete proteome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            215 AA; 23582 MW; D314CF7225F8A983 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 7; DB 1
Pred. No. 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Pred. w..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Search completed: September 26, 2003, 17:37:19
Job time: 26.0681 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3.56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 100.
nes 7; Conservative
                                                                                                                                Nature 390:249-256(1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         120 VALSLFL 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10 VALSLFL 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
        STATE AND SERVICE OF STATE OF 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30
```

us-09-852-100a-2_copy_68_269.rspt

```
QBV194 helicobacte
Q9x174 helicobacte
Q9x179 helicobacte
Q9x373 helicobacte
Q9x38 helicobacte
Q9x38 helicobacte
Q9x38 helicobacte
Q9x38 helicobacte
Q9x186 helicobacte
Q9x187 mycobacteri
Q9x1m6 pyrococcus
Q9x1m6 pyrococcus
Q9xy1 arabidopsis
Q9xy1 arabidopsis
Q8y176 mycoplasma
Q9xy1 arabidopsis
                 helicobacte
helicobacte
helicobacte
helicobacte
helicobacte
helicobacte
helicobacte
helicobacte
                                                                                                                                                                                 helicobacte
helicobacte
helicobacte
helicobacte
helicobacte
helicobacte
helicobacte
                                                                                                                                                                 helicobacte
helicobacte
                                                                                                                                                          helicobacte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 PSGPSAPEAVTARLVGVLWFVSVTTGPWGAVATSAGGEESLKCEDLKVGQYICKDPKIND
                                                                                                                                                                                                                                                                                                                                                                                                                    MEDELNE-21276355; PubMed-11278849; MEDELNE-21276355; PubMed-11278849; MEDELNE-21276355; PubMed-11278849; Malker S., Sofia H.J., Wang W., Kajkwaki E.M., Lo C.F., Ning X., Walker S., Ryan K., McHendry-Rinde B., Smith S.C., Wood A., Rhodes K.J., Kennedy J.D., Bard J., Hacobsen J.S., Ozenberger B.A.; "beter-amyloid Peptide-induced Apoptosis Regulated by a Novel Protein Containing a G Protein Activation Module."; Biol. Chem. 276:18748-18756(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                  Domo Transia. Buteleostomi.
Eukaryota, Metazoa Chordata, Craniata, Vertebrata, Euteleostomi.
Mammalia, Butheria, Primates, Catarrhini, Hominidae: Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .
0
                                                                                                                                               0893517
0933011 P
0933011 P
089371 P
089371 P
089365 P
089365 P
089365 P
089365 P
         O8vni8
                  09s3£1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 207;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Strausberg R.;
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AF353990; AAK35064.1; ·.
EMBL; BC029486; AAH29486.1; ·.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POTENTIAL.
A5590FD7AECDF292 CRC64;
                                                                                                                                                                                                                                                                                                                                01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 202; DB 4; I
Pred. No. 4.3e-205;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                207 AA
                                                                                                                                                                                                                                                                       AI, I GNMENTS
                                                                                            Q9AC92
Q8GG56
Q9V1M6
Q8EV17
Q9LXV9
Q8FU99
                                                                                                                                                                                                                                                                                                                 PRT;
                         08VLG4
09S3F4
08VNF9
09S3F0
09S3F3
                                                                    08VL58
09R3S8
09S3E9
                                                                                                                                               Q8VN51
Q93CN1
Q8VN49
Q8GK71
                                                                                                                                                                                                           Q8GK66
Q8GK65
Q8GK64
                                                                                                                                                                                          08CK68
08GK67
         C8VNT8
C9S3F1
                                                                                                                                                                                                                                   Q8GK63
                                                                                                                                                                                   08GK70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 37 PC
207 AA; 22326 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.0%;
Matches 202; Conservative 0.
                                                                                                                                                                                                                                                                                                                                                          Beta-amyloid binding protein
                                                                                                                17
16
10
                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                             1141
1159
1159
1173
1173
                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
NCB1_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IISSUE-Testis;
                           SEQUENCE
                                                                                                                                                                                                                                                                                                                         09BX74;
                                                                                                                                                                                                                                                                                                                 Q9BX74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIGNAL
                                                                                                                                                                                                                                                                                              RESULT 1
C9BX74
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           093164 rhodovnlum
094651 homo sapiec
094156 mus musculu
09brn9 homo sapien
08bj83 mus musculu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               019496 caenorhabdi
09vcw7 drosophila
08cam1 mus musculu
08u581 agrobacteri
09s3f2 helicobacte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9bx74 homo sapien
Q99mb3 mus muscul
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QSh046 home sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          09w2hl drosophila
095qz5 caecorhabdi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        O9u4h5 drosoph:la
                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                    (without alignments)
497.069 Million cell updates/sec
                                                          September 26, 2003, 17:29:43; Search time 104.868 Seronds
                                                                                                              PSGPSAPEAVTARLVGVLWF.....TRLTRLSITNETFRKTQLYP 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Description
                                                                                                                                                                                           830525
        GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                        Total number of hits satisfying chosen parameters.
                                                                                                                                                        830525 seqs, 258052604 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUMMARIES
                                                                                            US-09-852-100A-2_COPY_68_269
                                           - protein search, using sw model
                                                                                                                                                                                                                                    Post-processing: Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  095025
093164
09H651
09H651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q8CAM1
Q8U581
Q9S3F2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9BX74
Q99MB3
Q9H046
                                                                                                                              OLIGO
Gapop 60.0 , Gapext 60.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                086183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q19496
Q9VCW7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9BRN9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       09C4H5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q9W2H1
                                                                                                                                                                                                                                                           sp_archea:*
sp_hacteria:*
sp_furg1:*
sp_furg1:*
sp_human:*
sp_invertcbrate:*
sp_mammal:*
sp_mammal:*
sp_organelle:*
                                                                                                                                                                                                                                                                                                                                                                            sp_unclassified:*
                                                                                                                                                                                                                                                                                                                                                          sp_virus:*
sp_vertebrate:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 G
                                                                                                                                                                                                                                                                                                                                                                                    sp_rvirus:*
sp_bacteriap:*
                                                                                                                                                                                                           Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                     sp_archeap:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          111
                                                                                                                                                                                                                                                                                                                                                   sp_rodent:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query
Match Length DB
                                                                                                                                                                                                                                                                                                                                          sp_plant:*
                                                                                                                                                                                                                                                     SPTREMBL_23:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                207
208
80
1178
1178
1195
220
221
247
247
261
284
1638
1638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0004444444444444
                                                                                                                                                                                                                                                                                                                                         110...
                                                                                                                                                                        0
                                                                                                                                                                                                                                                                                              Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score
                                                                                                                              Scoring table:
                                                                                                                                                                        Word size :
                                           OM protein
                                                                                                                                                                                                                                                     Database :
                                                                                                                                                        Searched:
                                                                                                                Seguence :
                                                            Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Result
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .
9
```

ó

9

<del>2</del> ò q ò a ó Ω

Gaps

ن:

0; Indels

Length 80;

```
And MEDELINE-20196606; Pubbkod=10731132;
Addams M.D. Celniker S. E., Holt R. A., Evans C.A., Gocayne J.D.,
Addams M.D. Celniker S. E., Holt R. A., Evans C.A., Gocayne J.D.,
Addams M.D. Celniker S. E., Holt R. A., Exhormer M., Henderson S.N.,
Bandatides P.G., Scherer S.E., Lip P. W., Hoskins R. A., Galle R. F.
Bandatides P.G., Scherer S.E., Holt G., Nelson C.R., Miklos G.L.G.,
Bardon R.C., Rogers Y.-H.C., Blazel R.G., Champe M., Pfeiffer B.D.,
Ann K.H. Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
Ballew R.M., Baud A., Baxendale J., Andrews-Flannchoch C. Baldwin D.,
Ballew R.M., Benos P.V., Bernam B.P., Bhandari D., Beasley E.M.,
Berkova D., Botchen M.R., Bouck J., Brokstein P., Bortkier P.,
Ballew R.M., Benos P.V., Bernam B.P., Bhandari D., Bolshakov S.,
Berkova D., Botchen M.R., Bouck J., Brokstein P., Brotkier P.,
Borkova D., Botchen M., Dougo L.E., Downes M., Dugan Rochas S., Pleischman I..,
R. Bottis R.C. Busam D.A., Buller H., Cadieu E., Center A., Chandra I.,
R.A. Cherry J.M., Caving S., Mays A.D., Dew I., Dietz S.M.,
R.A. Cherry J.M., Caving S., Mays A.D., Dew I., Dietz S.M.,
R.A. Glodek A., Gong F., Gorrell J.J.H., Gu Z., Gelbart W.M., Gabziellan A.E., Garg N.S., Gelbart W.M., Malcohn E.,
Aniali M., Kalush F., Kargen G.H., Ke Z., Kennison J.A., Martei B., McInteon G.H., Ke Z., Kennison J.A., Martei B., McInteon G.H., Ke Z., Kennison J.A., Nature J.M., Nalson K.A., Nixon K., Nusskern D.R., Parler M., Nalson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
Rabor D.R., Nelson K.A., Nixon K., Wang A.H., Wang X.,
Rabort S.M., Woy M., Wurphy B., Wurphy L., Wang Q.H., Wang S., Yao, Q.A.,
Syler Sas R., Tector C., Turner R., Venter E., Wang A.H., Wang A.H., Wang A.H., Wang C.Y., Wang C.Y., Worlder S.W., Wollyen M., Strong R., Sin E.,
Syler S., Syler E., Sylen H., Zhong F. Waller S.M., Wallen G., Schocher F., San C., Schocher F., Schocker F., Schocker F., Schong S., Shon W., Zhong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Arthropoda; Haxapoda; Insecta; Pterygota;
Neoprera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
Noenrer K., Beyer A., Mewes H.W., Weil B., Wiemann S.: Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases EMBL, A.512689; CAC21647.1; -- Hypothetical protein.
                                                                                                                                8BE6BE788235C58D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         61-MAY-2000 (TrEMBLrel. 15, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DFC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                          DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                  178 AA.
                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                 Pred. No.
                                                                                                                                                                          4.0%; Score 8;
100.0%; Pred. No
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Drosophila melanogaster (Fruit fly).
                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                   80 AA; 8699 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Science 287:2185-2195(2000)
[2]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CG10795 protein (LD27358P).
                                                                                                                                                   Guary Match
Bost Local Similarity Tuber
and 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                               130 GADRFYIG 137
                                                                                                                                                                                                                                                                                                        33 GADRFYLG 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIRAIN-BERKELEY
                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CG10795
                                                                                                                                                                                                                                                                                                                                                                                                                                       09W2H1:
                                                                                                                                                                                                                                                                                                                                                                                                                  Q9W2H1
                                                                                                                                                                                                                                                                                                                                                                           RESULT 4
                                                                                                                                                                                                                                                                                                                                                                                             09W2H1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AN RANGE SO
                                                                                                                                                                                                                                                                   8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          104 KPISCRNVNGYSYKVAVALSLFLGWLGADRFYLGYPALGLLKFCTVGFCGIGSLIDFILE 163
                                                                                                                121 ALSLFLGWLGADRFYLGYPALGLLKFCTVGFCGIGSLIDFILISMQIVGPSDGSSYIIDY | 187
                                                65
                                                6 PSGPSAPEAVTARL/VGVLWFVSVTTGPWGAVATSAGGEESLKGEDLKVGQYLGKDPK1ND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 110 KPISCRNVNGYSYKVAVALSLFLGWLGADRFYLGYPALGLLKFGTVGFCGISS...PFI...
                                                                                         61 ATQEPVNCTNYTAHVSCFPAPNITCKDSSGNETHFTGNEVGFFKPISCRNVNGYSYKVAV
                         Kajkowski E.M., Lo C.F., Ning X., Walker S., Sofia H.J., Wang W., Edris W., Chanda P., Wagner E., Vile S., Ryan K., McHendry-Rinde B. Smith S.C., Wood A., Rhodes K.J., Kennedy J.D., Bard J., Jacobsen J.S., Ozenberger B.A.;
"beta-Amyloid Peptide-induced Apoptosis Regulated by a Novel Protein Containing a G Protein Activation Module.":
EMBL, AF353993, AAK35067.1: -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata; Euteleostemi,
Mammalia; Eutheria; Primates, Catarrhini; Hominidae; Homo.
NCBL_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .
.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 208;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22271 MW; 91A7932163F4F04C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               164 SMQIVGPSDGSSYIIDYYGTRLTRLSITNETFRKTQLYP 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    170 SMQIVGPSDGSSYIIDYYGTRLTRLSIINETFRKTQLYP 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-WAR-2001 (TrEMBLrel. 16, Created)
01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-CCT-2002 (TrEMBLrel. 22, Last annotation update)
Hypothetical protein (Fragment).

DKFZP667C1011.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JUN-2001 (TrEMBLrol. 17, Created)
01-JUN-2001 (TrEMBLrol. 17, Last sequence update)
01-DEC-2001 (TrEMBLrol. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            49.0%; Score 99; DB 11; Le
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       80 AA
                                                                                                                                                                                                                                                                                                                                                                                                                  209 AA
                                                                                                                                                                                                                                                                                      YGTRLTRLSITNETFRKTQLYP 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-21276355; PubMed-11278849;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          49.00.
100.08; Pre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Beta-amyloid binding protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MGD; MGI:2137022; Bbp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 99; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         208 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. TISSUE-Lymph node;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-BALB/C:
                                                                                                                                                                                                                                                               181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  о9но46
О9но46;
                                                                                                                                                                                                                                                                                                                                                                                                                                         099MB3;
                                                                                                                                                                                                                                                                                                                                                                                                                  Q99MB3
```

RESULT 3 Q9H046

ŏ g ò  $\sim$ 

```
PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         190 APEAUTAR 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6 APEAVTAR 13
                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                           NCB1_TaxID=35806;
                                                              BchO (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=Muscle;
                                                                                                                                                                                                                     STRAIN-W4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q9H651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C9H65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ದ್ದ
    STANDER REPORTED OF STANDARD O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ..
:
                                                                                                                                                                                                                                                                                                 :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
              STRAIN=Berkeley:
Stapleton M., Brokstein P., Hong L., Adbayani A., Carlson J.,
Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
Gonzalez M., Guarin H., J. P., Liao G., Miranda A., Mingall C.J.,
Nunco J., Pacleb J., Paragas V., Park S., Phouanenavong S., Wan K.,
U. C., Lewis S.E., Rubin G.M., Celniker S.,
Submitted (OCT-2001) to the EMBL/Genbank/DDBJ databases.
EMBL, AR03453, AAR6720 1:
FMBL, AR05143; AAR6720 1:
FMBL, AR050343 CG010795.
SEQUENCE 178 AA, 19896 MW, 17C41166607ACC33 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    <u>ن</u>
                                                                                                                                                                                                                                                                                                 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Genome sequence of the nematode C. elegans: a platform for investigating biology, The C. elegans Sequencing Consortium.", Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                         Length 178;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4.0%; Score 8; DB 5; Length 195;
100.0%; Pred. No. 6.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    indels
                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gattung S., Maggi L.;
"The sequence of C. elogans cosmid C4:D:1.";
submitted (MAY-1997) to the EMBL/Genbank/JobBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases. EMBL: AF003740; AAL09331.1: -. HORMPep; C41D11.9; CE29489;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hypothelical protein.
SEQUENCE 195 AA; 21203 MW; 35945E407F184DAE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           095025;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence ::pdate)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical 21.2 kDa protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                         4.0%; Score 8; DB 5;
100.0%; Pred. No. 5.9;
ative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                206 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               195 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. 6.4
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=Bristol N2;
MEDLINE=99069613; PubMed=9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8; Conservative
                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Waterston R.; "Direct Submission.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 132 DRFYLGYP 139
                                                                                                                                                                                                                                                                                                                                                                            108 DRFYLGYP 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        130 GADRFYLG 137
                                                                                                                                                                                                                                    Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. STRAIN-Bristol N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-Bristol N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q93164
Q93164;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           095025
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C41D11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 6
Q93164
ID Q9316
AC Q9316
                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 5
Q95Q25
δ
                                                                                                                                                                                                                                                                                                                                                                            S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8
```

```
÷
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
TISSUE-small intestinc:
TISSUE-small intestinc:
Watchade R., Kumegai A., Liakura S., Yamazaki M., Tasniro H., Ota T.,
Suzuki Y., Obayashi M., Nishi T., Shibahara T., Tanaka T.,
Nakamura Y., Isogai T., Sugano S.;
Nakamura Y., Lisogai T., Sugano S.;
*NEDO human CDNA sequencing project.";
§ubmitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.

Kajkowski E.M., Lo C.F., Ning X., Walker S., Sotia H.J., Wang W.,

Rotis K., Chanda P., Wagner E., Vile S., Ryan K., McHendry-Rinde B.,

Smith S.C., Wood A., Rhodes K.J., Kennedy J.D., Bard J.,

Jacobsen J.S., Ozenberger B.A.,

"Beta-amyloid peptide induced apoptosis regulated by a novel protein
Containing a G protein activation module.";

J. Biol. Chem. 0:0-0(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matsuura K.;
Matsuura K.;
Matsuura K.;
In vivo electron transfer to the triheme cylochrome subunit bound to the photosynthetic reaction center complex in the purple bacterium Rhodoviuum sulfidophium.';
Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AB050579; BAB70691.1;
InterPro; IPR00073; AP_hydrolase.
InterPro; IPR00379; Ser_estrs_site.
Pfam: PF00561; abhydrolase; I.
PRINTS; PR00111: ABHYDROLASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryola, Metazoa, Chordara, Craniata, Vortebrata, Euteleostomi,
Mammalia: Eutheria, Primates, Catarrhini: Hominidae, Homo.
NCBI_IaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Yoshida M., Masuda S., Nagashima K.V., Vermeglio A., Stimada K.,
                                                                                                                                                                                    Rhodovulum sulfidophilum (Rhodobacter sulfidophilus).
Bacteria: Proteobacteria; Alphaproteobacteria: Rhodobacterales;
Rhodobacteraceae; Rhodovulum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 296;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      indeis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Strausberg R.;
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
EMBL: AR026257; BAB15415.1; -.
EMBL: AF335992; AAK35066.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8F6713A03BB5B076 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    09H651,
09H651,
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 22, Last annotation update)
01-0CT-2602 (TrEMBLrel. 22, Last annotation update)
Hypothetical protein FLJ22604 (BBP-like protein 2).
Cl-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4.0%; Score 8; DB 2;
100.0%; Pred. No. 5.7;
Live 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         221 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE 206 AA; 21900 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 100.0 Matches 8; Conservative
```

0

Gaps

ő

RESULT 8 **09D156** 

òλ 5

```
SEQUENCE FROM N.A.
STRAIN-CSTBL/GAJ; IISSUE-Forelimb;
MEDLINE-22354683; PubMed=12466851;
The FANTOM Consortium,
the FINEN Genome Exploration Research Group Phase I & II Team;
*Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Suteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleos.Lomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBL_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAY-2006 (TrEMBLrel. 13, Created)
01-MAY-2006 (TrEMBLrel. 13, Last sequence update)
01-MAY-2006 (TrEMBLrel. 13, Last sequence update)
01-MAY-2006 (TrEMBLrel. 23, Last annotation update)
01-MAX-06097974 (ALMONEX) (AMX protein).
AMX OF BEDDAS:GHOSTO (COL1212)
Drosophila melanogaster (Fruit fly).
Drosophila melanogaster (Fruit fly).
Neoptera: Endopterygota, Diptera; Brachycera; Muscomorpha;
NCBI_TAXID-7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 261;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                 Strausberg R.;
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC036150; AAH06156.1; -.
Hypotherical protein.
SEGUENCE 247 AA; 27161 MW; CEID0D9C53DDF73G CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nature 420:563-573(2002).
EMBL, AK077858, BAC37037.1; -
SEQUENCE 261 AA; 28880 WW; 70346780D3CF5CDB CKC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Greated)
Last sequence update)
Last annotation update)
                                     01-JUN-2001 (TrEMBLrel. 17, Last sequence update) 01-DEC-2001 (TrEMBLrel. 19, Last annotation update) Similar to hypothetical protein FLJ22604.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
4.0%; Score 8; DB 11;
Best Local Similarity 100.0%; Pred. No. 8.3;
Matches 8; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     261 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              284 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   / Malch 4.0%; Score 8; DB 4
Local Similarity 100.0%; Pred. No. 7.9
Hes 8; Conservative 0; Mismatches
        C1-JUN-2001 (IrEMBLrel. 17, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAR-2003 (TYEMBLRE], 23, 01-MAR-2003 (TYEMBLRE], 23, 01-MAR-2003 (TYEMBLRE], 23, 23, 21milar to BBP-like protein Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      130 GADREYLG 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    130 GADREYLG 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          214 GADRFYLG 221
                                                                                                                                                                      Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q904H5; Q9W361
                                                                                                                                                                                                                                                                                                                                                                                                            ::SSUE=Colon;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cuery Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9U4H5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 063383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 11
Q904H5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 10
C85J83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ŝ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OC OC OC OC OC OC
        SON SERVICE SON SE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SCREEN REPRESENTATION OF THE PROPERTY OF THE P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ô
                                                                                                                                                                                                                                                  ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-C57BL/63; TISSUB-Embryo;

A RAWAW J. Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

A Rawawa J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

A Azawa T., Hara A., Fukunishi Y., Konco H., Adachi J., Fukuda S.,

A Azawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

A Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

A Azawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

A Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Radota K., Matsuda H.A., Ashburner M., Batalow B., Kochiwa H.,

Radota K., Matsuda H.A., Ashburner M., Baldarelli R., Barsh G., Quackonbush S.,

A Rakai K., Okido T., Futuno M., Carninci P., de Bonaido M.F.,

Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaido M.F.,

Brownstein M.J., Bult C., Fletcher C., Fujita M., Cariboldi M.,

A Brownstein M.J., Bult C., Fletcher C., Fujita M., Cariboldi M.,

A Roshincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

A Nordone P., Rang B., Ringwald M., Rodriguez I., Sakamoto N.,

Sasaki H., Sato K., Kang K.H., Weitz C., Whittaker C., Wilming L.,

A Nymshaw Bootis A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

A Nymshaw Bootis A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Saps
                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniala, Vertebrata, Euteleostomi:
Mammalia, Eutheria, Rodentia, Sciuroquathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Functional annotation of a full-length mouse cDNA collection.":
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            :0
                                                                                                                                                                                                                                                  3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 230;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0: Indels
                                                                                                                                                                  Length 221
                                                                                                                                                                                                                                             0: Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Liscol.
Strausberg R.;
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AK003917; BAB23075.1; -.
EMBL; BC024620; AH24620.1; -.
MGD; MGI:1915884; 1110025109Rik.
SEQUENCE 230 AA; 25639 MK; 396D65CD8BEES9A5 CRC64;
                                                                                   221 AA; 24410 MW; 92151D6EF6363D74 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
1110025:0981k protein (RIKEN cDNA 1110025109 gene).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4.0%; Score 8: DB 11;
100.0%; Pred. No. 7.4;
ative 0; Mismatches
                                                                                                                                                          4.0%; Score 8; DB 4;
100.0%; Pred. No. 7.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      247 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                230 AA.
                                                                                                                                                                               100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
EMBL; BC008873; AAH08873.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nature 409:685-690(2001).
                                                                                                                                                              Query Match
Best Local Similarity 100.
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
TISSUE-Salivary gland:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     183 GADRFYLG 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   130 CADRFYLG 137
                                                                                                                                                                                                                                                                                                                                                                           130 GADRFYLG 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus (Mouse).
                                                  Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hayashizaki Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1110025109RIK.
                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9BRN9
Q9BRN9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9D156;
Q9D156;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 9
Q9BRN9
```

ö

Gaps

.: O

'n

```
PRELIMINARY;
                                                                                                                                                                                               Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     109 KDSSGNET 116
237 GADREYLG 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Direct Submission.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       86 KDSSGNET 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. STRAIN-Bristol N2:
                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. STRAIN-Bristol N2;
                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Waterston R.;
                                                                                                                                                                                 F16H11.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      O9VCW7
                                                   RESULT 12
019496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9VCW7
                                                                                               3
                                                                                                                                                                                                                                                                                                                 RX STATAL-BERKELEY,

RA Adams M.D. Celniker S.E. Holt R.A. Frans C.A. Gocayno J.D.,

RA Adams M.D. Celniker S.E. Holt R.A. Frans C.A. Gocayno J.D.,

RA Adams M.D. Celniker S.E. Holt R.A. Frans C.A. Gocayno J.D.,

RA Adams M.D. Celniker S.E. Holt R.A. Frans C.A. Gocayno J.D.,

RA George T. C. K. Scherer S.E. J. F.W., Hoskins R.A. Galze R.P.,

Sutron G.G. Wortman J.R. Yandell M.D. Zhaigo C. Chen L.X..

RA Brandon R.C. Beater E.G. Helt G. Welson C.R. Mixios G.L.G.

RA Abril J.F. Agbayani A. An H.-J. Andrews Frankoch C. Bealdwin D.

Ballew R.M. Beater B.V. Berman B.P. Bandari D. Bolshakov S.,

RA Borkova D. Botchan M.R. Bouck J. Brokstein P. Brottler P.

RA Borkova D. Botchan M.R. Bouck J. Brokstein P. Brottler P.

RA Bottls K.C. Husam D.A. Buller H. Cadleu E. Center A. Chandra I.

RA Bottls R. Doup L.E. Downes M. Dugan Rocha S. Dunkov B.C. Dunn F.

RA Bottl J.M. Canagelista C.C. Fortaz C. Ferricra S. Flesschman W.

RA Bottl M. J. Evangelista C.C. Fortaz C. Ferricra S. Flesschman W.

RA Harris N.L. Harvey D. Heiman T.J. Hernandez J.R. Houck J. A.

RA Harris N.L. Harvey D. Heiman T.J. Hernandez J.R. Houck J.

RA Harris N.L. Harvey D. K. Howland T.J. We M. Glasser K.

RA Harris N.L. Moy W. Mutphy B. Mutphy L. Mixiny D.M. Ncison D.L.

RA Harris N.L. Moy W. Mutphy B. Mutphy L. Mixiny D.M. Ncison D.L.

RA Harris N.L. Moy W. Mutphy B. Mutphy L. Mixiny D.M. Ncison D.L.

RA Shue B. D. Lei Y. Levitsky A.A. Li J.J. Bully Y. Rese M.G.

RA Shue B. C. Siden Kiamos J. Simpson M. Stupsky Wang S. Yan G.A.

RA Shue B.C. Siden Kiamos J. Simpson M. Stupsky B. Wang Z. Y. Wassarman D.A. Weissen D.C.

RA Shue B.C. Siden Kiamos J. Shun R. Zhong S. Zhu X. Smith H. Shing A. Hogen G. M. Wang Z. Y. Wassarman D.A. Weissen D.C.

RA Shue B.C. Siden Kiamos J. Shun M. Zhou X. Zhu S. Zhu X. Smith H. Shing A. Hogen G. W. Wang S. Yan G. Zhun G. J. Leng R. Shence 287 Jano G. Zhong S. Leng R. Shence S. S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
             SEQUENCE FROM N.A.
Rubin G.M., Wan K.H., Harvey D., Lewis S.E., Brokstein P., Tsand G., Apbayani A., Arcaina T.T., Baxter E., Blazei, R.G., Futchhoff C., Champe M., Chavez C., Chew M., Doyle C.M., Farfan D.E., Frise E., Gaile R., George R.A., Harris N.L., Hoskins R.A., Evans-Holm M., Houston K.A., Hummasti S.R., Kim E., Li P., Moshrefi M., Pacleb G.M., Ceiniker S., Sequeira A., Sethi H., Snir E., Svirskas R.R., Weinburg T., Ceiniker S.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 284;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                             "Full Length Drosophila melanogaster cDNA sequence.";
Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                "Characterization of almondex.";
Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FlyBase; FBg::0000077; amx.
InterPro; IPRO01304; Lectin_C.
PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
SEQUENCE 284 AA: 31364 MW; BFBBFFB5733ACB5] CRC64;
                                                                                                                                                                                                              TISSUE=Ovary;
Michellod M.-A.E., Remillieux N.C., Randsholt N.B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4.0%; Score 8; DB 5;
100.0%; Pred. No. 9;
1ve 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4.0°,
100.0%; Pre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL: AF181623; AAD554091; -. EMBL: AF217797; AAF36924.2; -. EMBL; AE003446; AAF46474.2; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                              STRAIN-BERKELEY
```

130 GADRFYLG 137

```
EMBL; 055376; AAA98005.1; ...

REMBL; 055376; AAA98005.1; ...

ROTHPEP: P2033; LA6Y.

ROTHPEP: PER000536; Hormone_rec_lig.

R InterPro; IPR0010528; Zf_C45teroid.

R Fram: PF001104; hormone_rec; 1.

R FRINIS; PR00045; Zf_C4; ...

R FRINIS; RA003430; Zf_C4; ...

R RART; SA003430; ADL_C4; ...

RWART; SA003430; ADL_C4; ...

KW Hypothetical protein: DNA-binding; Metal-binding; Nuclear protein; KW Receptor; Transcription; Transcription; Transcription; Zinc; Zinc; finger.

SEQUENCE 548 AA; 63545 MW; OBB5C51C6850BB96 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                        Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoldea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
-:- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
-:- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTOR FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        :
ن
                                                                                                                                                                                                                                                                                                                                                                                        "Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium."; Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Drosophija melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta: Pterygota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4.0%; Score 8; DB 5; Length 548;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "The sequence of C. elegans cosmid Fi6H11."; Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
01-NCV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical 63.5 kDa protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Pred. No. 17; ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT; 1638 AA
                                                                                                                                                                                                Rhabditidae, Peloderinae, Caenorhabditis.
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                 STRAIN-Bristol N2;
MEDLINE-99069613; PubMed-9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Rest Local Similarity 100.000
Feet Local Similarity 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CG6954 protein.
CG6954.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AC
DT
DT
DE
OC
OC
```

```
STRAIN-C57BL/6J; TISSUE-Hypothalamus; MEDLINE-22354683; PubMed-12466851; The FANTOM Consortium.
The FANTOM Consortium.
The RIKEN Genome Exploration Research Group Phase : 6 II Team; Analysis of the mouse transcriptome based on functional annotation of 60.770 full-length cDMAs..; Mature 420:563-573(202).
EMBL: AK038530: BAC30030.1; -...
                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutelcostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              38 AA; 4188 MW; 2DB363A494415D42 CRC64;
                         01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update
                                                                                                               LIM motif-containing protein kinase 2 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 100.
Les 7; Conservative
                                                                                                                                        Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 ALSLFLG 127
                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                  NCBI_TaxID-10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cuery Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q80581;
Q80581;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                080581
  SOUR PRANTS NO CONTRACTOR NO C
                                                                                                                                                                          RAM Adams N.D. Celniker S.E. Li P.W. Stans C.A., Goceyne J.D.,

RA Adams N.D. Celniker S.E. Li P.W. Stastics R.A., Galle R.F.,

RA Adams H.D. Celniker S.E. Li P.W. Stastics R.A., Galle R.F.,

RA George R.A., Lewis S.E., Holt R.A., Eashburner W., Henderson S.N.,

Ran Baradon R.C., Rogers Y.H.C., Blazel S.G., Champe M., Helffor b.D.,

RA Abril J.E., Agbayani A. An H.J. Andrews Pformacon C.R., Miklos G.L.G.,

RA Ballew R.W., Basu A., Baxendale J. Bayrakiaroqlu L., Beasley E.M.,

Ballew R.W., Basu A., Baxendale J., Bayrakiaroqlu L., Beasley E.M.,

Ballew R.W., Basu A., Baxendale J., Bayrakiaroqlu L., Beasley E.M.,

Ballew R.W., Cawley S., Daller H.J., Andrews Pformacon C.R., Miklos G.L.G.,

RA Burtis K.C., Busam D.A., Bouler H. Cadicu E., Center A. Chandro C. Cherry J.M., Cawley S., Daller H., Dever S.M.,

RA Burtis K.C., Busam D.A., Bouler H., Cadicu E., Center A., Chandro C. Cherry J.M., Cawley S., Daller H., Dever S., Diller R.A.

RA Geblos B., Delcher A., Bownes M. Digarn Rocha S., Pleischmann W. Delcher A., Goog F. C., Ferraz C., Gunn F.,

RA Harris N.L., Harvey S., Gorrell J.H., Gu Z., Gunn P., Harris M.,

RA Harris N.L., Harvey D., Helman T.C., Herrandez J.R., Houck J.,

RA Harris N.L., Harvey D., Helman T.C., Herrandez J.R., Houck J.,

RA Harris M.W., Multon C.D., Kraft C., Wravitz S., Kipp J., Lai Z.,

RA Multans B. E., Kodire C.D., Kraft C., Wravitz S., Kipp J., Lai Z.,

RA Multans M.W., Multoph B., Multoph L., Mulany D.M., Nelson D.H.,

RA Milanna D.M., Nelson K., Standers R.D.C., Scieeler F., Shor H.,

Spier E., Spradling A.C., Stapheton M., Stupsk: M.P., Smith H.C.,

RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weisseebach J.,

RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weisseebach J.,

RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weisseebach J.,

RA Wang S.M., Woodge T., Worley K.C., Wu D., Yang S., Yao C.A.,

RA Wang S.M., Woodge T., Worley K.C., Wu D., Yang S., Yao C.A.,

RA Wang S.M., Woodge T., Worley K.C.,

Ra Sheng S.M., Woodge T., Worley K.C.,

Ra Sheng S.M., Woodge T., Worley K., Wu D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gabs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 8; DB 5; Length 1638;
Pred. No. 45;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1638 AA; 180548 MW; 3CC84F9A24A9F5DC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                         Ephydroidea: Drosophilidae; Drosophila.
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE: PS50088; ANK_REPEAT; 1.
PROSITE; PS50297; ANK_REP_REGION; 1.
                                                                                                                                        STRAIN-BERKELEY;
MEDLINE-20196006; Pubmed-10731132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR002110; ANK.
InterPro; IPR003961; FN_ITI.
InterPro; IPR00159; RA_domain.
Pfam; PF00023; ank; 2.
Pfam; PF00041; fn3; 1.
Pfam; PF00788; RA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ouery Match
Best Local Similarity 100.
Matches 8, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SMART; SM00248; ANK; 1.
SMART; SM00060; FN3; 1.
SMART; SM00314; RA: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ANK repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SECUENCE
```

; 0

0; Indels

DB 11; Length 38;

3.5%; Score 7; DB 11 100.0%; Pred. No. 16; tive 0; Mismatches

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M., Qurollo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin I., Houmiel K., Gordon J., Vaudin M., Iartchouk O., Epp A., Liu F., Wollam C., Allinger M., Doughty D., Scott C., Lappas C., Markelz B., Flanagan C., Crowell C., Gurson J., Lomo C., Sear C., Sirub G., Cielo C., Slater S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ó,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Genome sequence of the plant pathogen and biotechnology agent. Agrobacterium tumefaciens {\sf C58."};
                                                                                                                                                                                                                                                                                              Agrobacterium tumefaciens (strain CSB / ATCC 33970).
Bacteria: Proteobacteria; Alphaproteobacteria; Rhizobiales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 16; Length 97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     97 AA; 10642 MW; 6B2B2E03D4137F36 CRC64;
                                                                                                                                                                                                  Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. 38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Pred. ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Search completed: September 26, 2003, 17:41:35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 7;
                                                                                                                                                                           Created)
                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE-21608551; PubMed-11743194;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Science 294:2323-2328(2001).
                                                                                                                                                                      01-JUN-2002 (TrEMBLrel, 21, 01-JUN-2002 (TrEMBLrel, 21, 01-JUN-2002 (TrEMBLrel, 21, AGR_C.3268p.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AEC08099; AAK87547.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity 100.
tes 7; Conservative
                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                    Rhizobiaceae; Rhizobium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8 EAVTARL 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      47 EAVTARL 53
3 ALSLFLG 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Job time : 106.868 secs
                                                                                                                                                                                                                                                                                                                                                                      NCB:_TaxID-176299;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ô
```

38 AA.

PRT;

PRELIMINARY;

Q8CAM1 RESULT 14 Q8CAM1 ID Q8

ô d

```
September 26, 2003, 17:22:38; Search time 97 Seconds (without alignments) 715.630 Million cell updates/sec
                                                                                                                                                              US-09-852-100A-2
1439
1 MHILKGSPNVIPRAHGQKNI.....TRLTRISITNETFRKIQIYP 269
                                                                                                                                                                                                                                                                                                                   830525
5.1.6
Compugen Ltd.
                                                                                                                                                                                                                                                                                                              Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                 830525 seqs, 258052604 residues
 GenCore version
Copyright (c) 1993 - 2003
                                                                                                                                                                                                                                                                                                                                                                                             Post-processing: Minimum Match 0%
Maximum Match 190%
Listing first 45 summaries
                                                                 OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sp_archea:*
sp_bacteria:*
sp_tung:*
sp_tung:*
sp_ivvertebrate:*
sp_manmal:*
sp_mho:*
sp_phage:*
sp_phage:*
sp_phage:*
sp_plant:*
sp_plant:*
sp_prodent:*
sp_vortebrate:*
sp_vortebrate:*
sp_vortebrate:*
sp_vortebrate:*
sp_vortebrate:*
sp_vortebrate:*
sp_vortebrate:*
sp_vortebrate:*
                                                                                                                                                                                                                                 BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sp_rvirus:*
sp_bacteriap:*
sp_archeap:*
                                                                                                                                                                                                                                                                                                                                                 Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                SPIREMBL_23:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99...
112...
115...
175...
                                                                                                                                                               Title:
Perfect score:
Sequence:
                                                                                                                                                                                                                                    Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Database :
                                                                                                                                                                                                                                                                                 Searched:
                                                                                                Run on:
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Q9bx74 homo suplen	Q99mb3 mus musculu	09w2hl dresophila	Q95pj8 caenorhabdi	Q9h651 homo sapien	Q9brn9 homo sapten	O8bj83 mus musculu	Q9d156 mus muscelu	Q9u4h5 drosophila	Q9h046 homo sacien	Q95qz5 caenorhabdi	Q9bx73 homo sapien	Q9vy85 drosophila		Q8n0x9 homo sapien	
SUMMAKIES	QI,	Q9BX74	O99MB3	Q9W2H1	Q95PJ8	09н651	Q9BRN9	Q8BJ83	090156	Q9U4H5	09H046	095025	Q9BX73	Q9VY86	O9BSR6	6X0N80	098022
	DB	4	::	2	2	4	4	Π	Ξ	Ŋ	4	'n	7	2	4	4	7
	% Query Match Length DB	207	208	178	329	221	247	261	230	284	80	195	214	172	149	171	106
	% Ouery Match	77.3	65.4	23.5	19.3	13.9	13.9	13.8	13.6	12.6	12.0	11.8	9.5	8.7	8.4	8.4	8.1
	Score	1113	941.5	338	278	200	200	198.5	196	182	172	169.5	136.5	125	121	121	117
	Result No.	г	7	m	4	2	φ	7	8	6	10	11	12	13	14	15	16

17 115	5.5	8.1	213	11	Q9CWL9	ans
œ	ى. ت	۲.	2.3		08R014	C8r0i4 mus musculu
2	5.5	٦.	213	11	Q8BJJ1	Q8bjjl mus muscula
O	107	4.	106	16	08F808	O8f808 leptospira
1	5.5	٣.	142	16	Q8DJB9	
7	105	٣.	68	~	098015	
~	104	7.	159	9		Q8fu99 corynebacte
24	86	ω.	1092	S		
25	4	7.	137	9		C932pl staphylococ
9	S)	9.	913		075061	075061 homo sapien
۲,	95	9.	309		C9RS03	Q9rs03 deinococcus
ъ ъ	$\sim$	₹.	9/	ø	Q8EVR7	Q8evr7 mycoplasma
6	92	₹.	456	12	Q66668	8
0	92	₹.	720	S	Q9V5W4	
1	85	4.	720	ហ	Q961T2	
2	91	٣.	1324	12	09J3E7	~
m	90.5	٣.	151	11	Q8K181	Q8k181 mus musculu
~*	90	m.	204	10	Q8R2E7	
5	5.5	.2	069	10	022512	
9	89	7.	330	12	098339	
7	88	۲.	1324	12		
8	7.5	٠٠.	400	16		
.8 68	87.5	۲.	547	16	Q9R2J4	Q9rzj4 deinococcus
0	7.5	۲.	1207	'n		
7	87	0.	1274	10		
42	87	0.	1321	12		Q9j3f1 murine hepa
80	è.		364	ហ	Q9VXJ5	77
4 8	e.		7	16	×	S
80	9		æ	17	Q978F6	
					ALIGNMENTS	
RESULT 1						
093X74						
ID Q9BX74		PRELIMINARY	NARY;		PRT; 207 AA.	
AC 09BX74						
DT 01-JUN-2001	-2001	_		17,	Created)	
	-2001	)		17,	sednence nt	
	-2002	$\overline{}$	е Г	22,	Last annotation update)	
	myloid	binding	ď	otein	نـ	
BBP						
	sabiens	(Human)				
OC Eukary	ota; M	Eukaryota; Metazoa;		Ja ti	Craniata: Vertebrata;	steleostoms;
	ia; Eu	ther ia;	Primates;	ate	Catarrhini, Hominidae;	Ното.

. O

63 MAAAWPSGPSAPEAVTARLVGVLWFVSVTTGPWGAVATSAGGEESLKCEDLKVGQYICKD 122

ò

Q99MB3

099MB3

qq ò g

ò

qq ò

Mus

ò q ò Ω ò q ô g

```
REALIN-BERKELEY,

RAM AMEDIIND-20196006, PubbHed-10731132;

RAM AMEDIIND-20196006, PubbHed-10731132;

RAM AMADAIGES S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RAM George R.A., Lewis S.E., Li P.W., Hoskins R.A., Galle R.F.,

Sutton G.G., Mortman J.R., Yandell M.D., Zhaig O., Chen L.X.,

RAM Abril J.E., Agbayari A., Baxter E.G., Helt G., Nelson C.R., Mikios G.L.G.,

RAM Abril J.E., Agbayari A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

Ballew R.M., Basu M., Baxendale J., Bayraktaroglu L., Beasley E.M.,

RAM Abril J.E., Agbayari A., Am H.-J., Addrews-Ffannkoch C., Baldwin D.,

RAM BOKOVA D., Borcham R.P., Bouck J., Brokstein P., Brottler P.,

RAM BOKOVA D., Borcham R.P., Doug C., Morstein P., Brottler P.,

RAM BOKOVA D., Borcham R.P., Doug Z., Mays A.D., Dew I., Dietz S.M.,

RAM BOKOVA D., Doup L.E., Downes M., Dugan Rocha S., Pleischman W.,

RAM BOKON K., Cawley S., Dahlke C., Davenport L.B., Davies P.,

RAM BOKON K., Cawley S., Dahlke C., Daven P.,

RAM BOKON K., Cabbiellan A.E., Garg N.S., Gelbart W.M., Glasser K.,

RAM Glodek A., Gong F., Gorrell J.H., Well M.-I., Ibeyamm C.,

RAM Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,

RAM Harris N.L., Harvey D., Heiman T.J., Well M.-I., Ibeyamm C.,

RAM Abail M., Kalush F., Karpen G.H., Ke Z., Kunison J.A., Kectchum K.A.,

Jalai M., Kalush F., Karpen G.H., Kerl Y., Kennison J.A., Kectchum K.A.,

Jalai M., Kalush F., Karpen G.H., Ke Z., Kunison J.A., Mattei B.,

Mount S.M., Moy M., Murphy E., Murphy L., Worley W., Sin E.,

Svirskas R., Medie B., McIntosh T.C., McLeod M.P., Weissenbach J.,

Ram B.E., Spradling A.C., Stapleton M., Stupski M.P., Smith T.,

Spier E., Spradling A.C., Stapleton M., Stupski M.P., Wang Z., Yu, Wassarman D.A., Wang Z., Yu, Wassarman D.A., Wang S., Zhu X., Smith H.S.,

Shies B.C., Siden-Kamos I., Simpson M., Stupski M., Shor S., Zhu X., Smith H.S.,

Steinec 267.2165-2195(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                107 SLKCEDLK-VGQYICKDP---KINDATQEPVNCTNY-TAHVSCFPAPNITCKDSSGNETH 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      162 FIGNEVGFFKPISCRNVNGYSYKVAVALSLFLGWLGADRFYLGYPALGLLKFCTVGFCGI 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20 NVDCNELQMMGQFMCPDPARGQIDPKTQQLAGCTREGRARVMCIAANEINCTE-TGNAT-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Stapleton M., Brokstein P., Hong L., Agbayani A., Carison J.,
Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
Nunco J., Pacleb J., Paragas V., Park S., Phouanenavong S., Wan K.,
Yu C., Lewis S.E., Rubin G.M., Celniker S., Phouanenavong S., Wan K.,
Submitted (COT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AR001453; AAF467201.
                                          Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 5; Length 178;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17C41166607ACC03 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4.9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23.5%; Score 338; DB 5 42.6%; Pred. No. 3e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                42.6%; Pred. no.
                          Drosophila melanogaster (Fruit fly)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FBgn0034626; CG10795.
178 AA; 19896 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=Berkeley;
                                                                                                                                                                                    STRAIN-BERKELEY;
                                                                                                               NCBI_TaxID-7227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FlyBase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
  Ś
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        111 YKVAVALSLELGWLGADRFYLGYPALGELKFCTVGFCGIGSLIDFILISMGIVGPSGGSS :80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DPKINDATQEPVNCINYTAHVSCFPAPNITCKDSSGNETHFTGNEVGFFKPISCRNVNGY 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63 MAAAWPSGPSAPEAVTARLVGVLWFVSVTTGPWGAVATSA-GGEESLKCEDLKVGGYICK 12;
                                                                    PKINDATQEPVNCTNYTAHVSCFPAPNITCKDSSGNETHFTGNEVGFFKPISCRNVNGYS 182
                       1 MAAAWPSGPSAPEAVTARLVGVLWFVSVTTGPWGAVAISAGGBBSI.KCBDI.KVGQYICKD 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        183 YKVAVALSLFLGWLGADRFYLGYPALGLLKFCTVGFCGIGSLIDFILISMQIVGPSDGSS
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-BALB/C;
MEDLINE-2126355; PubMed-11278849;
MEDLINE-2126355; PubMed-11278849;
Kajkowski E.M., Lo C.F., Wing X., Walker S., Sofia H.J., Wang W.,
Edris W., Chanda P., Wagner E., Vile S., Ryan K., McHendry-Rinde H.,
Smith S.C., Wood A., Rhodes K.J., Kennedy J.D., Bard J.,
Jacobsen J.S., Ozenberger B.A.;
"beta-Amyloid Peptide-induced Apoptosis Regulated by a Novel Protein
Containing a G Protein Activation Module.";
EMBL, AF351993; AAK35067.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota: Metazoa; Chordata; Craniata; Vertobrata; Eutelecstomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    65.4%; Score 941.5; DB 11: Length 208; 85.1%; Pred. No. 8.4e-79; cive 16: Mismatches 20; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22271 MW; 91A7932163F4F04C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (TrEMBLrel. 13, Created)
(TrEMBLrel. 13, Last sequence update)
(TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SYIIDYYGTRLTRLSITNETFRKTQLYP 269
                                                                                                                                                                                                                                                   243 YIIDYYGTRLIRLSITNETFRKTQLYP 269
                                                                                                                                                                                                                                                                           Beta-amyloid binding protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 09W2H1;
01-WAY-2000 (TEMBLEE]. 13,
01-MAY-2000 (TEMBLEE]. 13,
01-DEC-2001 (TEMBLEE]. 19,
CG10795 protein (LD27358P).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 85.1 Matches 177; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MGD; MGI:2137022; Bbp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         208 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID-10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                            181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Duery Match
```

Q9W2H1

RESULT 3

ò g

```
135 CINYTA--HVSC----FPAPNITCKDSSGNETHFTGNEVGFFKPISCRNVNGYSYKVAVA 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     135 CTNYTA--HVSC----FPAPNIICKDSSGNETHFIGNEVGFFKPISCRNVNGYSYKVAVA 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              189 LSJFLGWLGADRFYLGYPALGLLKFCTVGFCGIGSLIDFILISMGIVGPSDGSSYI 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           189 LSLFLGWLGADRFYLGYPALGLLKFCTVGFCGIGSLIDFILISMQIVGPSDGSSYI 244
             Kajkowski E.M., Lo C.F., Ning X., Walker S., Sofia H.J., Wang W., Edris W., Chanda P., Wagner E., Vile S., Ryan K., McHendry-Rinde B., Jack S.C., Wood A., Rhodes K.J., Rennedy J.D., Bard J., Josenberger B.A.; Betta-amyloid peptide-induced apoptosis requlated by a novel protein containing a G protein activation module."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBL_TaxID-9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 13.9%; Score 200; DB 4; Length 247; Best Local Similarity 45.7%; Pred. No. 2.4e-10; Matches 53; Conservative 12; Mismatches 39; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                      13.9%; Score 200; DB 4; Length 221; 45.7%; Pred. No. 2.1e-10; tive 12; Mismatches 39; Indels
                                                                                                                                                                                                                                                              Submitted (MAY-2001) to the EMBL/GemBank/DDBJ databases. EMBL: AK026257; BAB15415.1; -. EMBL: AR353992; AR435066.1; -. EMBL: BC008873; AR480873.1; -. Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Strausberg R.:
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BCJ06150; AAH06150.1; -.
Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             i protein.
247 AA: 27161 MW; CEIDGD9C53DDF73C CRC64;
                                                                                                                                                                                                                                                                                                                                                                               221 AA; 24410 MW; 92151D6EF6363D74 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Similar to hypothetical protein FLJ22604.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   261 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23,
23,
23,
                                                                                                                                                                                                                                                                                                                                                                                                 Ouery Match Best Local Similarity 45... best Local Similarity 65...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q8BJ83;
01-MAR-2603 (TrEMBLrel.
01-MAR-2003 (TrEMBLrel.
01-MAR-2003 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
                                                                                                                                                                                                   SECUENCE FROM N.A.
                                                                                                                                                                                                                     TISSUE-Muscle;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE-Colon;
                                                                                                                                                                                                                                                 Strausberg R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C9BRN9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   083383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 7
Q8BJ83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QSBRN9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         á
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98 VATSAGGEESLKCEDLKVGQYICKDPKINDATQEPVNC-TNYTAHVSCFPAPNITC--KD 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            155 SSG--NETHFTGNEVGFFKPISCRNVNGYSYKVAVALSLFIGWLGADRFYLGYPALGHUR 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        70 QFGIFNRT------VPSACHYGAHVSYTTIVIL.SIFLGFFGIDKIYLGYYALGLIK 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ŝ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUB-Small intestine;
Watanabe K., Kumagal A., Itakura S., Yamazaki M., Tashiro H., Ota T.,
Suzuki Y., Obayashi M., Nishi T., Shibahara T., Tanaka T.,
Nakamura Y., Isogai T., Sugano S.;
"NEDO human cDNA sequencing project.";
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Khabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Enteleostomi:
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    213 FCTVGFCGIGSLIDFILLSMQIVGPSDGSSYIIDYYGTRLTRLSIINETFRK 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           120 MFSI.GGLEVEWLVDIII.ISLQLLGPADGTAYAMAYYGDKAQMIRLVATINKK 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19.3%; Score 278; DB 5; Length 329; 36.6%; Pred. No. 2.2e-17; ive 34; Mismatches 59; Indeis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genome sequence of the nematode C.elegams: A platform for
                    GSLIDFILISMOIVGPSDGSSYIIDYYGTRLTRISTTNETFR 263
                                           Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  investigating biology.";
Science 282:2012-2018(1998).
EMBL. ALI61712. CAC35892.1;
WormPep: 765012A.21; CE26465.
SEQUENCE 329 AA: 38167 MW; 9C5FB3EE7E386650 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Hypothetical protein FLJ22604 (BBP-11ke protein 2).
                                                                                                                                                                                                                                          Last sequence update)
Last amotation update)
                                                                                                                                                                                                                       Created)
                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        [2]
SEQUENCE FROM N.A.
MEDLINE-99069613; Pubmed-9851916;
                                                                                                                                                                                                              63; Conservative
                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                               Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID-6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sulston J.E.
                  222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                       Q95PJ8
Q95PJ8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9H651
Q9H651;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                              RESULT 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 5
                                                                                                                                                  095PJ8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    09H651
```

ô g δ qq ö d 'n

PACO OC OCT SERVING CONTRACT SERVING CON

5

Gaps

```
221 IGSLIDFILISMOIVGPSDGSSYI 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              149 NITCKDSS------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       59; Conservative
                                                                                                                                                                             Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                 TISSUE-Salivary gland;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-BERKELEY;
                                                                                                          Hayashizaki Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9U4H5; Q9W361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ::SSUE-Ovary;
                                                                                                                                                                                                                                                                                                                Strausberg R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          090485
          RRARRA BRANCORRA BRANCORRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 े
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    급
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ÷
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kawai J., Shinagawa A., Shibata K., Yoshino M., Itch M., Ishii Y.,
A Arakawa I., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
A Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
A Saito T., Okazaki Y., Golobori T., Bono H., Kasukawa T., Saito R.,
A Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant I.,
A Kuchi P., Lewis S., Matsuo Y., Nikaido I., Pesolo G., Quackenhush J.,
A Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner I., Washio T.,
A Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner I., Washio T.,
A Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
A Brownstein M.J., Buit C., Fletcher C., Fujita M., Gariboldi M.,
A Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mochaerts P.,
A Lyons P., Marchionni L., Mashima J., Mazzarelli J., Sakamoto N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   46 LLGGGGSGSGEKVSVSKMAAAWPSGPSAPEAVTARLVGVLWFVSVTTGPWGAVATSAGGE 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          106 ESLKCEDLKVGQYICKDPKINDAIGEPVNCTNYTAHVS------CFPAPNTTCKDS 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    71 ----ESTEIPPYMIKCPSNGLCSRLPADCIECAINVSCIYGKPVIFDCTVKPSVTCVDQ 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TAL MENDIER : 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                126 DLKPORNFVINMICRECWOLPETDYECSNSTIGMIVACHRORYFANCIVRDHISCLGNRS 185
                                                                                                                                                                                                                               STRAIN-CS7BL/63; TISSUE=Forelimb;
MEDLINE=2235468: PubMed=12466851;
The FANTOM CONSORtium.
The FANTOM CONSORtium.
The FANTOM CONSORTIUM.

"Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length coNRs.";
Nature 420:563-573(2002).
EMBL; AK077858: BAC37037.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26 ILSGDGSLNLEHSGPLAQAIKDP-GPTRTFSVVPRAAENQLFSHLT-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GFFKPISCRNVNGYSYKVAVALSLFLGWLGADRFYLGYPALGLIKFCTVGFCG16S1.15F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   79; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota: Metazoa; Chordata: Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi: Muridae; Murinae; M:s.
NCBL_TaxID=10090;
                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Eutoleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 11: Length 251;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                261 AA; 28880 MW; 70346780D3CF5CDB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence updatc)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
1110025109Rik protein (RIKEN CDNA 1110025109 gene).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   86:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----GNET-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13.8%; Score 198.5; DB L
26.8%; Pred. No. 3.5e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23: Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN-C57BL/6J; TISSUE-Embryo;
MEDLINE-21085660; Pubmed_1121785;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       228 lliSMQIVGPSDGSSYI 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LIGVGYVCPADGSLYI 261
Similar to BBP-like protein 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       69: Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse).
                                          Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                          SEQUENCE FROM N.A
                                                                                                                                          NCBI_TaxID-10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 156 S-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1110025IC9RIK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9D156;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             951060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QΩ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          á
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Db
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACCOOR NOTE THAT THE PROPERTY OF THE PROPERTY 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ô
```

```
102 AGGEESL.---KCEDLKVGQYICKDPKINDATQEPVNCTNYTAHVS------CFPAF 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          86 SVICVDQDLKPQRNFVINMICRFCWQLPETDYECSNSTTCMIVACPRORYFANCIVRDHI 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 161 HFTGNEVGFFKPISCHNVNGYSYKVAVALSLFLGWLGADRFYLGYPALGLIKFCTVGFCG 220
Sasaki H., Sato K., Schoenbach C., Seya I., Shibata Y., Storch K.-F., Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L., Wynshaw Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28 SEDENOLESHLTESTEIPPYMTKCPSNGLCSRLPADCIECATNVSCTYGKPVTFDCTVKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
Rubin G.M., Wan K.H., Harvey D., Lewis S.E., Brokstein P., Tsang G., Agubin G.M., Wan K.H., Harvey D., Lewis S.E., Brokstein P., Tsang G., Agubin A., Arcaina T.T., Baxter E., Blazej R.G., Butenhoff C., Champe M., Chavez C., Chew M., Doyle C.M., Farfan D.E., Frise E., Galle R., George R.A., Harris N.L., Hoskins R.A., Evans-Holm M., Houston K.A., Hummasti S.R., Kim E., Li P., Moshrefi M., Pacleb J.M., Park S., Sequeira A., Sethi H., Snir E., Svirskas R.R., Weinburg T., Celniker S.E.;
"Full Length Drosophila melanogaster CDNA sequence."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                               'Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-20196006; Pubmed-10731132;
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
AMAN OR BODAN.GHO2974 (ALMONDEX) (AMX protein).
AMX OR BODAN.GHO2974 OR CG12127.
Drosophila melanogaster (Fruit fly).
Bukaryota, Metazoa; Arthropoda; Hexapoda; Insenta; Pterygota;
Bohydroidea; Endopterygota; Diptera; Brachycera; Muscomorpha;
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 230;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ---GNET-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     64; Indeis
                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (MRR-2002) to the EMBL/GenBank/DDBJ databases EMBL; AK003917; BAB23075.1; -. EMBL; BC024620; AAH24620.1; -. MGD; MGI.191584; Ill0025109Rik. SEQUENCE 230 AA: 25639 WW; 396D650D8BEE99AS CHC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Michellod M.-A.E., Remillieux N.C., Randsholt N.B.; "Characterization of almondex.":
Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13.6%; Score 196; DB 11; 28.9%; Pred. No. 5e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     284 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19; Mismatches
```

```
Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. STRAIN*Bristol N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-Bristoi N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A
                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID-6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Waterston R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hypothetical
                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C41D11.9
                                                                                                                                                                                                              Ouery Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                           095025
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 11
                                                                                                                                                                                                                             Best
                                                                                                                                                                                                                                                                                                                                                                                                                                           095025
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SSEEREFEERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                          D,
                                                                                                                                                                                                                                                                                                                                              õ
RA Amanatides P.G., Scherer S.E., Li P.W., Scklus R.A., Galle K.E.,
RA George R.A. Lewis S.E., Richards S., Ashburner M., Henderson S.R.,
Brauton G.G., Wortman J.R., Yandell M.D., Champe M., Profitor B.D.,
RA Brandon R.C., Rogers Y. H.C., Riazej R.G., Champe M., Profitor B.D.,
RA Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Kiklos S.L.G.,
RA Ballew R.M., Basu A., Baxter E.G., Helt G. Nelson C.R., Kiklos S.L.G.,
RA Ballew R.M., Basu A., Baxndale J., Bayraktarcelu I., Bassley E.M.,
RA Ballew R.M., Basu A., Baxndale J., Bayraktarcelu I., Bassley E.M.,
RA Burkis K.C., Busam D.A., Butler H., Cadlew E. Contex A., Clandra I.,
RA Burkis K.C., Busam D.A., Butler H., Cadlew E., Contex A., Clandra I.,
RA Burkis K.C., Busam D.A., Butler H., Cadlew E., Poncise P.
RA Geblos B. Delcher A., Dency Z., Mays A.D., Dew I.D. Dietz S.W.
RA Dodson K., Downe M., Downort L.B., Dawies P. P., Frieschmin W. RA
Loubin K.J., Evangelista C.C., Forraz C., Ferriara S., Fleischmin W.,
RA Hostrie N.L., Harvey D., Heiman T.J., Herrandez C.R., Fleischmin W.,
RA Hostrie N.L., Harvey D., Heiman T.J., Herrandez C.R., Ketchur K.A.,
Alali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchur R.A.
Alali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchur R.A.
Alali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchur R.A.
Alali M., Moy M., Murby B.D., Murby L., Murchy J., Moshreti A.,
RA Alazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Resee P.G.,
RA Reinert K., Remington K.S., Junchy S., Shor E.,
Shue B.C., Suden Kiamos I., Slupskin M., Strong R., Shue B.C., Suden Kiamos I., Slupskin P., Murch S., Musi A., Wang X.,
RA Shirsa R., Tector C., Turner R., Venter E., Wang A., Musi R.,
RA Mang Z.-Y., Wasserman D.A., Weinsenbach J.,
RA Shore R.A., Robing T., Wonder S., Zhu X., Shith H.O.,
RA Zheng X.H., Zhong F.N., Robing G.M., Weissenbach J.,
Rhe Gener S., Suden Kiamos I., Shong W., Venter J.C.,
Rhe Gener S., Shong S., Shong S., Zhu X., Shith H.O.,
Rhe Fenner S., Shong S., Shong S., Shong S.,
Rhe Gener S., Shong S., Shong S., S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       104 GEESLK------CEDLKVGQYICKDPKINDATQEPVNCTNYTAH--VSCFPAANITCKD 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       155 SSGNETHFTGNEVGFFKPISCRNVNGYSYKVAVALSLFLGWLGADRFYLGYPALGILKFC 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        205 --GNRS-FTRN------LRCNWTQGYRWSTALL/SLTLGGFGADREYLGHWQRG1GK3F 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        154 GERSFØRØMNCRYCYQTEMWOQSCGQRSSCNSATDKIJFRTNCTVHHDVI,CI,------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Cramiata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 284;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        51; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InferPro, TPR001304; Lectin_C.
PROSITE: PS00615; C_TYPE_LECTIN_1: 1.
SEQUENCE 284 AA; 31364 MW; 8FFBFFB5733AC851 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OPHO46:
01-MAR-2001 (ITEMBLEE). 16, Created)
01-MAR-2001 (ITEMBLEE). 16, Last sequence update)
01-OCT-2002 (ITEMBLEE). 22, Last annotation update)
Hypothetical protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 182; DB 5;
Pred, No. 1.3e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      215 TVGFCGIGSLIDFILISMQIVGPSDGSSYI 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL: AF181623; AAD55409.1; -.
EMBL: AF217797; AAF36924.2; -.
EMBL: AE003446; AAF46474.2; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       33.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 33.3%
Watches 50; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEOUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FlyBase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 10
Q9H046
            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
```

```
157 GNETHFTGNEVGFFKPISCRNVNGYSYKVAVALSLFLGWLGADRFYLGYPALGLLKFCTV 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          104 GEESLKCE---DLKVGQYICKDPKINDATQE----PVNCINYTA------HVSCF 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             146 PAPNITCKDS-----SGNETHFTGNEVGFFKPISCRNVNGYSYKVAVALSLFLGWLGA 198
                                                                                                                                                                                                                                                                                                                                                                                                                                             34 GSAGLTCTFPGDCRIGDIV----KVNCTSRKGCPNPVSRNNVEAVCRFCWQLLPGDYDCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota: Metazoa; Nematoda; Chromadorea; Rhabdit.ida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                               ..
œ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium."; Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11.8%; Score 169.5; DB 5; Length 195; 28.9%; Pred. No. 1.1e-07;
Manualia; Butheria; Frimates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                               DB 4; Length 80;
                                                                                                                                                                                                                                                                                                                                                               30; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "The sequence of C. elegans cosmid C41D11.";
Submitted (MAX-1997) to the EMSL/GenBank/DDB3 databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          <u>..</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases. EMBL; AF003740; AAL08031.1; -. WormPep; C41D11.9; CE29489.
                                                                                                        Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases. Hypothetical north 1; -- Introduction of the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             il protein.
195 AA; 21263 MW; 35945E407F184DAE CRC64;
                                                                                                                                                                                                                                                                8BE6BE788235C58D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          _
_
=
:
                                                                                                                                                                                                                                                                                          Score 172; DB 4,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ş
                                                                                                                                                                                                                                                                                                                                                               9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 217 GFCGIGSLIDFILISMQIVGPSDGSSYI 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGLGIWTLIDVLI,IGVGXVGPADGSLYI 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-99069613; PubMed-9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hypothetical 21.2 kDa protein.
                                                                                                                                                                                                                                                                80 AA; 8699 MW;
                                                                                                                                                                                                                                                                                                               12.08;
                                                                                                                                                                                                                                                                                                                                          46.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        48; Conservative
                                                                                                                                                                                                                                                                                                                                                               41; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-Bristol N2;
Gattung S., Maggi L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'Direct Submission.";
```

ø

```
Adams M.D.,
   ã
                                                                                                                                                                                                                                                                                                                                                                                                                                         SVSKMAAAWP----SGPSAPEAVTARLVGVLWFVSVTTGPWGAVATSAGGEES--LKCED 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     113 LKVGQYICKDP--KINDAT--QE-PVNCTNYTAH-----VSCFPAPNITCKDSSGN 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             76 LPDEFIECEDPVDHVGNATASQELGYGCLKFGGQAYSDVEHTSVQCHALDGIEC---ASP 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RTFLREN-----KP--CIKYIGHYFIITLLYSFFLGCFGVURFCLGHTGTAVGKILTILGG 185
90 PATHCSTSSTKLLVTKCSAHSSVICHGQRNFYKRIPCNWSSGYSWTKTMILSVVLGGEGA 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                              SHSQNATAEPELISAGAAQPE-----GPGGAASWEYGDPHSPVILGSY 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    159 ETHFIGNEVGFFKPISCRNVNGYSYKVAVALSIFLGWLGADRFYLGYPALGILKFCIVGF
                                                                                                                                                                                                                                                                                                                                                                                                                   Indels 47; Gaps
                                                                                                                                                                                                                                                                      Kajkwwski E.M., Lo C.F., Ning X., Walker S., Sofia H.J., Wang W., Edris W., Chanda P., Wagner E., Vile S., Ryan K., McHendry-Rinde B., Smith S.C., Wood A., Rhodes K.J., Kennedy J.D., Bard J., Jacobsen J.S., Ozenberger B.A., "beta-Amyloid Peptide-induced Apoptosis Regulated by a Novel Protein Containing a G Protein Activation Module.";
J. Biol. Chem. 276:19748-19756(2061).
SEMBL. AFS35991; AAK35065.1; - SEQUENCE 214 AA, 22871 MM; BB928712AF2F78A8 CRC64;
                                                                                                                                                                                                    Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostemi:
Mammalia; Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Socayne J.D.,
                                                                                                                                                                                                                                                                                                                                                                                          9.5%; Score 136.5; DB 4; Length 214; 27.8%; Pred. No. 0.00014;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygeta;
                        199 DRFYLGYPALGLIKFCTVGFCGIGSLIDFILISMQIVGPSDGSSY1 244
                                      Neoptera: Endopterygota: Diptera: Brachycera: Muscomorpha:
Ephydroidea: Drosophilidae: Drosophila.
NCBL_TaxID=7227;
                                                                                                                                                                                                               Catarrhini; Nominidae;
                                                                                                                                           Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                   83.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                         Owery Match
9.5%; Score 1:0.0.
Best Local Similarity 27.8%; Pred. No. 0.000
Matches 58; Conservative 21; Nismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    172 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  219 CGIGSLIDFILISMQIVGPSDGSSYIIDY 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LGIWWFVDLILLITGGLMPSDGSNWCIVY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAY-2000 (TrEMBLrel, 13, Created)
01-OCT-2002 (TrEMBLrel, 22, Last seq
01-OCT-2002 (TrEMBLrel, 22, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cc11103.
Drosophila melanogaster (Fruit fly).
                                                                                                                                Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                       PRT;
                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE-21276355; PubMed-11278849;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-20196006; PubMed-10731132;
                                                                                                                              01-JUN-2001 (TrEMBLrel. 17, 01-JUN-2001 (TrEMBLrel. 17, 01-MAR-2003 (TrEMBLrel. 23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CG11103 protein (LP03404p).
                                                                                                                                         01-JUN-2001 (TrEMBLrel.
01-MAR-2003 (TrEMBLrel.
BBP-like protein 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                         PRELIMINARY;
                                                                                                                                                                                         (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-Berkeley:
                                                                                                                                                                                                                         NCBI_TaxID=9606;
                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                        59
                                                                                                                                                                                                                                                                                                                                                                                                                                                               33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          196
                                                                                                                    09BX73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98YV9Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               09VY86;
                                                                                                       Q9BX73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 13
                                                                                RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98YY86
                                                                                            09BX73
                                                                                                                    οý
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                              a
                                                                                                                                                                                                                                                                                                                                                                                                                                                              임
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                        õ
```

```
Mannalides PG. Scholers E. H. 18 N. Hockens R.A. Galle R.F.,
AN SILOGE G. M. Wortzan J. B. Lichards S. Asabharas R.A. Galle R. F.
Bendon N. C., Regers Y. H.C. Blazej R.G. Tchampe M., Felffer B.D.
Ann I. J. Abbayani A., An H.J. Andrews Ffannkohl C. Balduin D.
Ann I. J. F. Abbayani A., An H.J. Andrews Ffannkohl C. Balduin D.
Ann I. J. F. Abbayani A., An H.J. Andrews Ffannkohl C. Balduin D.
Ann I. J. F. Abbayani A., An H.J. Andrews Ffannkohl C. Balduin D.
Ann I. J. F. Abbayani A., An H.J. Andrews Ffannkohl C. Balduin D.
Ann I. J. F. Abbayani A., An H.J. Andrews Ffannkohl C. Balduin D.
Ann I. J. F. Abbayani A., An H.J. Andrews Ffannkohl C. Balduin D.
Ann I. J. F. Abbayani A., An H.J. Andrews Ffannkohl C. Balduin D.
Ann I. J. B. Abbayani A., An H.J. Andrews Ffannkohl C. Balduin D.
Ann I. J. B. Abbayani A., An H.J. Andrews Ffannkohl C. Balduin D.
Andrews F
```

,

```
Query Match
Best Local Similarity
Matches 42; Conserve
                                                                                                                                  SEQUENCE FROM N.A
                                                                                                       NCBI_TaxID +9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       101 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Job time
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Search
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ď
   d
                                                                                                                                                                                                                                                                                                                                                                                                                                                        õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        126 CKDP--KINDAI--QE-PVNCINYTAH-----VSCFPAPNITCKDSSGNETHHIGN 165
                                                                                                                                                                                                                                                                              120 CKDP-------KINDATQEPVN----CTNYTAHVSCEPAPNIICKDSS 156
                                                                                                                                                                                                                                                                                                                                      157 GNETHFTGNEVGFFKPISCRNVNGYSYKVAVALSLÆRGMIGADRFYLGYPALGLIKFCTV 216
                                                                                                                                                                                                                                                                                                                                                       166 EVGFFKPISCRNVNGYSYKVAVALSLFIGWLGADRFYLGYPALGLZKFCTVGFCGIGSLI 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18 CEDPVDHVGNATASQELGYGCLKFGGQAYSDVEHTSVQCHALDGIEC---ASPRIFLEEN
                                                                                                                                                                                                                                                                                                         41 CKDPVDHRENATAQQEKKYGCLKFGGSTYBEVEHAMVWCTVF-ADIECY------
                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                       Stapleton M., Brokstein P., Hong I., Aghayani A., Carlson C., Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E., George R., Gonzalez M., Guarín H., Kronmiller B., Li P., Liao G., Miranda A., Mungali C.J., Nanoo J., Pacleb J., Paragas V., Park S., Patel S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.X., Celniker S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bukaryota: Metazoa; Chordata; Cramiata: Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24;
                                                                                                                                                                                                                                                    42;
                                                                                                                                                                                                                    8.7%; Score 125; DB 5; Length 172; 25.9%; Pred. No. 0.0012; tive 18; Mismatches 49; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 121: 58 4: Length 149: Pred. No. 0.3024;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           60; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Straubberg R.;
Straubberg R.;
Submitted (MAR-2001) to the EMEL/GenBank/DDBJ databases.
EMBL: BC004878; AAH04878.1; -.
SEQUENCE 149 AA: 16490 MW; 7450105740B2A518 GROK4;
                                                                                                                              Submitted (JUN-2002) to the EMBL/GenBank/1003J databases EMBL; AE003493; AAF48318.2; --
BMBL; AT19007; AAM50867.1; --
FlyBase: Figno030522; CG11103.
SEQUENCE 172 AA: 18809 MW: 73DFFB4B1P780E39 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUN-2501 (TrEMBLrel. 17, Created)
01-JUN-2501 (TrEMBLrel. 17, Last sequence update)
01-MAR-2603 (TrEMBLrel. 23, Last annotation update)
Similar to RIKEN CDNA 2410018G23 gene.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Æ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 171
                                                                                                                                                                                                                                                                                                                                                                                                                  142 GGVGVWWIIDVILLITUNLLPEDGSNW 168
                                                                                                                                                                                                                                                                                                                                                                                                217 GFCGIGSLIDFILISMQIVGPSDGSSY 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      128 DLILLITGGLMPSDGSNWCTVY 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         226 DFILISMQIVGPSDGSSYIIDY 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match
Best Local Similarity 29.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             42; Conservative
                                                                                                                                                                                                                                   Best_Local Similarity 25.9
Matches 38; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
TISSUE-Pancreas;
[6]
SEQUENCE FROM N.A.
                              STRAIN-Berkeley;
                                                                                                                                                                                                                                                                                                                                                                 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             08N0X9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9BSR6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 09BSR6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 15
QBNOX9
ID QBNOX9
AC QBNOX9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q9BSR6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  οχ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Dp
Dp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ô
RRA RRA DR RRA DR RRA DR RRA DR RRA DR RRA DR DR DR DR SO
                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                           ΩD
                                                                                                                                                                                                                                                                                                                                                                 qq
                                                                                                                                                                                                                                                                                                                                                                                                                           q
                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                ô
```

```
Unionized (Trembline) 22. Created)

To 10-007-2002 (Trembline) 23. Last sequence update)

To 10-007-2002 (Trembline) 23. Last sequence update)

EWORDHERICAL Protein FLJ90546 (Hypothetical protein FLJ90674).

By Chimano Sapiens (Humano)

C. C. Mannalia: Eutheria: Primates; Catarrhini: Hominidae: Homo.

C. Mannalia: Eutheria: Primates; Catarrhini: Mannalia: Eutheria: Primates; Catarrhini: Hominidae: Homo.

R. Sucuri Y. Magai K. Sagano S. Ishlis. K. Adasi Hido Y. Saito K. Samania: Catarrhini: Catarrhini: Mannalia: Eutheria: Catarrhini: Catarrh
```